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ASSESSMENT OF ANTIMICROBIAL RESISTANCE BURDEN AND MULTIDRUG RESISTANCE DYNAMICS IN CLINICAL BACTERIAL ISOLATES

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Abstract
The development of antimicrobial resistance remains a serious issue in healthcare, since it reduces the efficacy of treatment and complicates the process of treating bacterial infection. Multidrug resistance plays an important role because of its potential impact on the selection of therapy and antibiotic stewardship programs. The present study assessed antimicrobial resistance burden and multidrug resistance dynamics in clinical bacterial isolates and examined their association with clinical outcomes. A quantitative retrospective secondary data analysis was conducted using 2,200 clinical isolate records. Variables included age, gender, specimen type, susceptibility results for five antibiotics, resistance genes, test method, and clinical outcome. Susceptibility categories were converted into resistance scores, and multidrug resistance was defined as resistance to at least three tested antibiotics. Descriptive statistics, chi-square tests, one-way ANOVA, binary logistic regression, and Pearson correlation analysis were performed at a significance threshold of $p < 0.05$. The mean age was 45.65 ± 26.27 years, with nearly equal gender distribution. Blood was the most common specimen type. VIM was the most frequent resistance gene, followed by OXA-48. Meropenem showed the highest resistance frequency, while colistin showed the highest sensitivity frequency. Multidrug resistance was identified in 20.55% of isolates. MDR status was not significantly associated with gender, specimen type, test method, resistance genes, or clinical outcome. The resistance score did not differ significantly across outcome groups. Logistic regression showed no significant mortality predictors, while MDR status correlated moderately with total resistance score. The burden of antimicrobial resistance was clear from high levels of multidrug resistance (MDR) and varied patterns of resistance genes. Mortality could not be predicted by the resistance burden alone.

Keywords: *antimicrobial resistance, multidrug resistance, clinical isolates, resistance genes, antibiotic susceptibility*

1. Introduction

One of the major issues in modern healthcare is antimicrobial resistance (AMR), which leads to decreased efficacy of antimicrobial agents. Growing antimicrobial tolerance in microorganisms complicates infection control procedures and leads to higher morbidity and mortality rates (Tang et al., 2023). Increased AMR levels pose additional risks to patients' health, especially among critically ill and immunocompromised individuals. AMR is associated with inappropriate use and abuse of antibiotics within medical practice, veterinary science, the agricultural industry, and environmental systems. Inappropriateness of antimicrobial administration promotes AMR and spreads resistance determinants in pathogenic strains. Some additional determinants of AMR include inappropriate infection control measures, self-medication, improper antibiotic prescribing habits, and incomplete therapeutic regimens (Ahmed et al., 2024). It should also be noted that AMR can be especially prevalent in healthcare environments with insufficient diagnostic and surveillance tools to detect resistant organisms. The negative effect of AMR is not limited to bacteria's capability of resisting medication action. Resistant infections are characterized by increased morbidity and mortality rates, extended periods of hospitalization, and higher financial burdens, since patients with AMR require special treatment regimes (Dadgostar, 2019). With a further increase in resistance, AMR will lead to serious problems in infection management.

Existing epidemiological data clearly illustrate the growing problem of AMR. Based on the results of a systematic study, bacterial AMR was estimated to account for 1.27 million deaths worldwide in 2019 (Murray et al., 2022). Similar collaboration studies have found that AMR is a prominent factor in mortality within various healthcare settings around the world (Antimicrobial Resistance Collaborators, 2022). This information emphasizes the growing importance of regular AMR surveillance for supporting public health efforts and improving antibiotic stewardship. Another aspect related to the impact of AMR is the increased spread of MDR pathogens. MDR organisms are resistant to multiple antimicrobial drug classes. Such pathogens are especially common among hospitalized patients and critically ill patients, who are at risk of developing MDR infections (Salam et al., 2023). Persistence of bacteria carrying resistance mechanisms leads to the occurrence of healthcare-associated infections. Dissemination of antibiotic residues in the environment is yet another aspect that contributes to AMR (Serwecińska, 2020). In this regard, AMR can be viewed as an interdisciplinary issue that includes aspects related to clinical medicine, environmental sciences, and public health. In light of this, comprehensive surveillance is necessary to identify the sources of resistance spread.

It is also known from previous investigations that MDR is a major problem that affects numerous bacterial pathogens and various therapeutic fields. Major factors leading to decreased efficacy of antimicrobial drugs include enzyme-mediated inactivation, efflux pumps, target-site alteration, and reduced cell membrane permeability (Catalano et al., 2022). High prevalence of MDR pathogens leads to serious difficulties with clinical identification and selection of adequate medications. Due to this fact, it becomes necessary to utilize reserve antibiotics and newer medications for overcoming resistance. Treatment of infections caused by MDR Gram-negative pathogens is especially problematic, owing to the lack of sufficient antibiotic alternatives and inferior clinical outcomes. Recent novel antibiotics were demonstrated to be potentially effective against resistant pathogens, but their application success still depends on susceptibility testing and proper antimicrobial selection (Kanj et al., 2022). However, some alternative methods, such as bacteriophage therapy, antimicrobial peptides, and antibiotic combinations, have been discussed as potential treatments against MDR organisms (Vivas et al., 2019). At the same time, AMR surveillance is critical for identifying trends in bacterial susceptibility and changes in resistance dynamics. According to clinical research, MDR pathogens have been shown to be related to higher ICU admission rate, ineffective therapy, and increased mortality among critically ill patients (Karruli et al., 2021). AMR burden will differ depending on bacterial genus, sampling site, local drug prescribing habits, and healthcare-associated transmission patterns. Treatment of Gram-positive and Gram-negative bacterial infections can be particularly challenging within healthcare settings characterized by high antibiotic usage (Kulkarni et al., 2019).

However, even though AMR and MDR were widely researched in the literature, many important gaps were identified. For example, most studies focus on single pathogens, particular resistance genes, or specific patient populations, while far fewer research projects have examined multiple aspects of AMR, including antibiotic resistance, gene presence, MDR status, and outcome of clinical treatment (Alara & Alara, 2024). Moreover, no studies paid enough attention to the evaluation of AMR burden with the help of cumulative resistance scoring methods.

For this reason, the present study was performed in order to investigate AMR and MDR dynamics among clinical bacteria. The aim of this project is the evaluation of antibiotic resistance levels, distribution of resistance genes, prevalence of multidrug resistance among isolates, and the relationship between MDR-related variables and clinical outcomes, including mortality.

2. Methodology

2.1 Research Design

The methodology used for this research involved an exploratory quantitative approach by applying a secondary data set in determining AMR profiles and multi-drug resistance status, along with its consequences. This research mainly relied on statistical testing of relationships between resistance profile and demographic or clinical factors.

2.2 Data Source

The data set used for the analysis was sourced from a freely accessible antibiotic resistance monitoring data set that was formulated by Siam et al. (2025). The data set includes information about patient demographics, type of sample,

antimicrobial susceptibility tests, antibiotic resistance genes, test methodologies used, and other relevant clinical outcomes for AMR surveillance. There were 2,200 observations and 12 variables in the data set.

2.3 Study Variables

The variables under investigation comprised demographic variables like age and sex, microbial variables such as sample type and resistance genes, and the results of antibiotic susceptibility testing against Amoxicillin, Ciprofloxacin, Meropenem, Vancomycin, and Colistin. The clinical outcomes of interest comprised ICU admission, recovery, and death. In order to enable statistical analysis, the antibiotic susceptibility results were quantified using resistance scores, where sensitive, intermediate, and resistant reactions were assigned scores of 0, 1, and 2, respectively.

The resistance score of each isolate was then calculated by adding up the resistance scores of all the antibiotics tested. Multidrug resistance (MDR) was categorized according to resistance to at least three classes of antimicrobial agents. Isolates that qualified for this category were marked as MDR, whereas all other isolates were labeled as non-MDR.

2.4 Data Processing and Cleaning

After data processing, variable names were standardised to facilitate the process of analysing the data. Missing values, duplicate values, and invalid susceptibility values were reviewed before proceeding to analyse data using statistical analysis techniques. Data for categorical variables were formatted, while missing resistance gene values were coded "Not Detected." Finally, numerical data were reviewed for any inconsistencies before calculating derived values like total resistance scores.

2.5 Statistical Analysis

Descriptive statistics were employed to describe demographics, distribution of specimens, drug resistance profile, antimicrobial susceptibility testing, and proportion of MDR. For all categorical variables, frequencies and percentages were reported, while mean and standard deviation were determined for continuous variables.

A chi-squared test was carried out to determine any relationship between the status of MDR and categorical clinical variables. One-way ANOVA was applied to compare the total resistance score among clinical outcome categories. Logistic regression was applied to determine factors affecting mortality from age, sex, status of MDR, and total resistance score as the predictors of mortality.

In addition, Pearson's correlation analysis was also used to find any association among demographic factors, status of MDR, total resistance score, and mortality. Statistical significance was considered at $p < 0.05$.

3. Results

3.1 Demographic and Clinical Characteristics of the Study Population

The number of patient records analyzed totaled 2,200. The average age of the study population was 45.65 ± 26.27 years (Table 1). The number of female subjects was 1,110 (50.5%) compared to males at 1,090 (49.5%). Specimen type distribution showed relatively equal occurrence among all groups, with blood specimens occurring the most (20.41%), followed by sputum and wound swab specimens (20.36%) and stool specimens (19.18%) (Figure 1). Results indicated that ICU admission was the most common outcome in 35.23% of cases, with mortality occurring in 31.18% of patients (Figure 2).

Table 1. Demographic and clinical characteristics of the study population

Variable	Category/Statistic	Frequency (%)
Age	Mean ± SD	45.65 ± 26.27
Gender	Female	1110 (50.45)
	Male	1090 (49.55)
Specimen Type	Blood	449 (20.41)
	Sputum	448 (20.36)
	Wound swab	448 (20.36)
	Urine	433 (19.68)
	Stool	422 (19.18)
Clinical Outcome	ICU	775 (35.23)
	Recovered	739 (33.59)
	Deceased	686 (31.18)

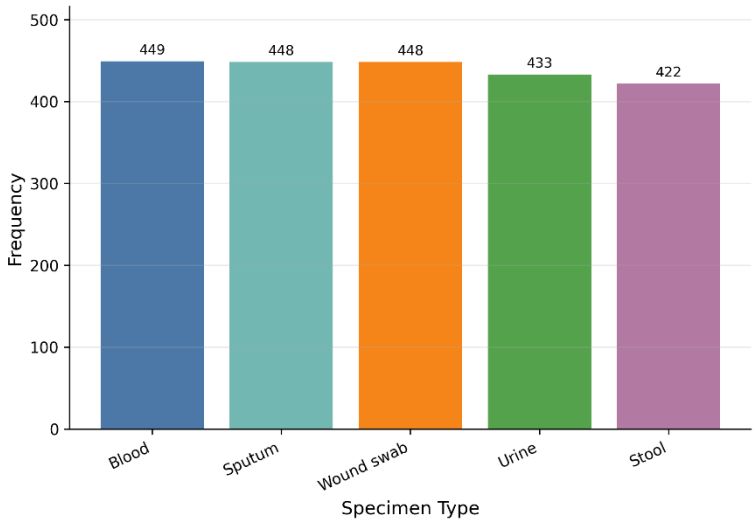

Figure 1. Distribution of specimen types

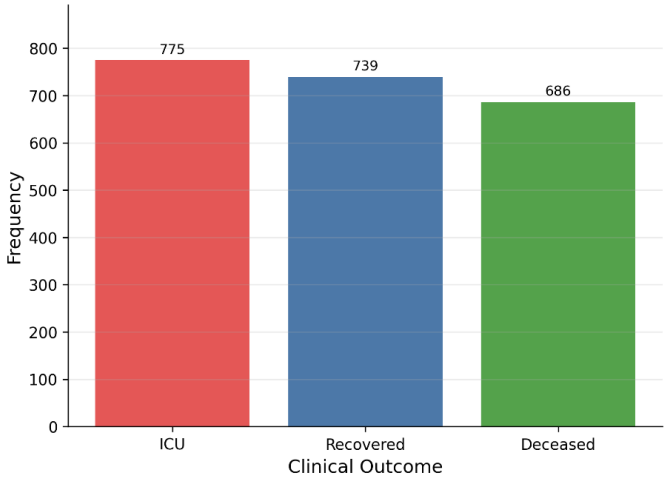

Figure 2. Clinical outcome distribution

3.2 Distribution of Resistance Genes and Antibiotic Susceptibility Patterns

Of the resistance genes that were found, VIM was the most common, being found in 463 (21.05%) isolates, while OXA-48 was present in 450 (20.45%) isolates. The KPC and NDM-1 resistance genes had similar prevalences, at 19.32% each, while there was an absence of any detectable resistance gene in 19.86% of the isolates (Figure 3).

The antibiotic susceptibility patterns revealed considerable differences among the antimicrobials used. Colistin had the highest sensitivity to antibiotics, with 761 isolates being sensitive, while Meropenem had the highest resistance rate, with 755 isolates being resistant. All antibiotics had intermediate susceptibility patterns (Figure 4).

\Table 2. Distribution of resistance genes and antibiotic susceptibility patterns

Resistance Gene	Frequency	Percentage (%)
VIM	463	21.05
OXA-48	450	20.45
Not Detected	437	19.86
KPC	425	19.32
NDM-1	425	19.32

Table 3. Distribution of Antibiotic Susceptibility Patterns

Antibiotic	Sensitive	Intermediate	Resistant
Amoxicillin	726	744	730
Ciprofloxacin	752	730	718
Meropenem	708	737	755
Vancomycin	757	726	717
Colistin	761	738	701

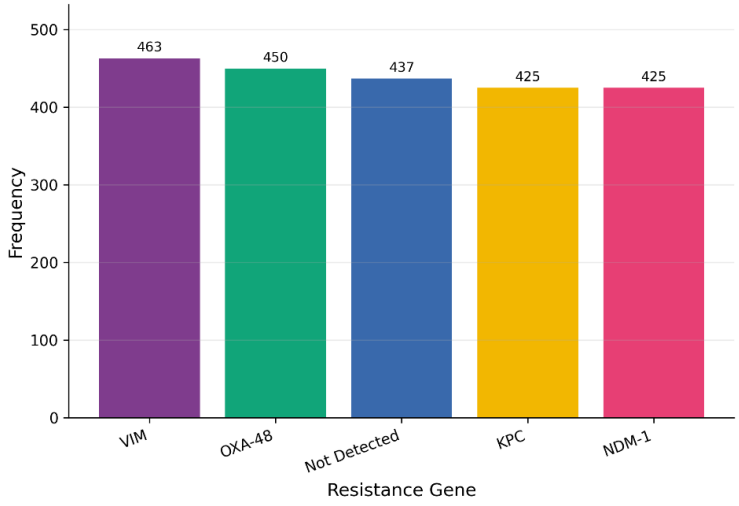

Figure 3. Distribution of resistance genes

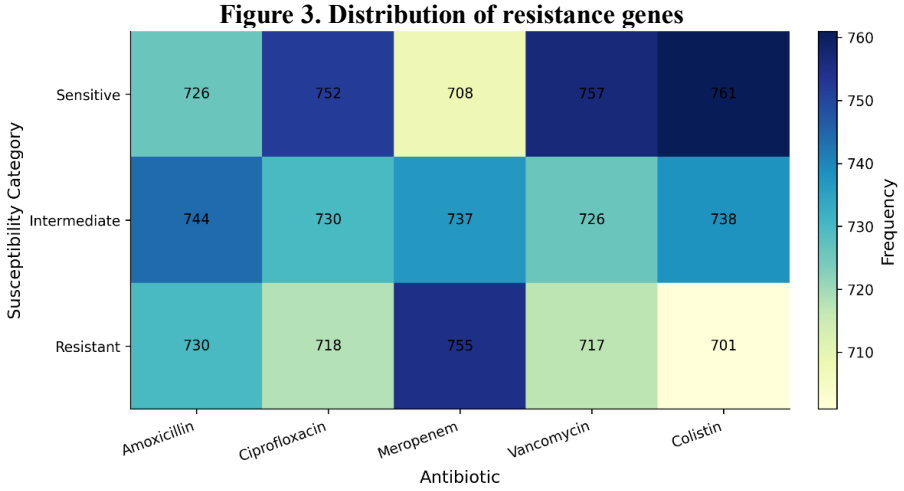

Figure 4. Antibiotic susceptibility heatmap

3.3 Distribution of Multidrug Resistance Status

The number of multidrug-resistant isolates was 452 (20.55%), while 1,748 (79.45%) isolates fell into the non-MDR group. Most bacterial strains were not multidrug-resistant, meaning that they remained susceptible to three or more groups of antimicrobials (Table 4, Figure 5).

Table 4. Distribution of multidrug resistance status

MDR Status	Frequency	Percentage (%)
Non-MDR	1748	79.45
MDR	452	20.55

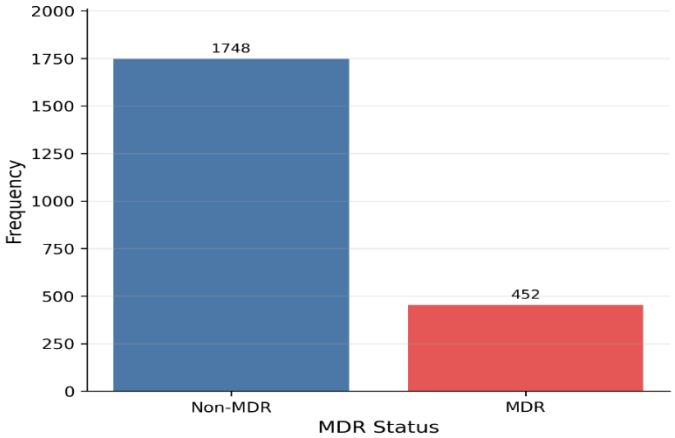

Figure 5. Distribution of MDR status

3.4 Association Between MDR Status and Clinical Variables

The chi-square test showed no statistically significant association between MDR status and gender (p=0.796), type of specimen (p=0.525), laboratory testing method (p=0.622), resistance genes (p=0.880), or patient outcome (p=0.510) (Table 5). These results suggest that MDR cases occurred evenly among demographics and clinical variables in the sample under examination.

Table 5. Chi-square association between MDR status and categorical variables

Variable	Chi-square	Degrees of Freedom	P-value
Gender	0.0666	1	0.796334
Specimen Type	3.2010	4	0.524770
Test Method	0.9487	2	0.622304
Resistance Genes	1.1898	4	0.879772
Outcome	1.3474	2	0.509830

3.5 Resistance Burden Across Clinical Outcomes

Resistance scores were fairly uniform between different clinical outcomes (Table 6, Figure 6). Patients who survived had a slightly higher mean resistance score (5.01 ± 1.81) than those in the ICU (4.95 ± 1.80) and patients who died (4.92 ± 1.83). However, one-way ANOVA analysis found no statistically significant variation of resistance burden between the three groups (F = 0.531, p = 0.588).

Table 6. Resistance score distribution across clinical outcomes

Outcome	N	Mean Resistance Score	SD	Minimum	Maximum
Deceased	686	4.915	1.826	0	10
ICU	775	4.955	1.798	0	10
Recovered	739	5.014	1.815	0	9

Note: F-statistic: 0.5310, P-value: 0.588084

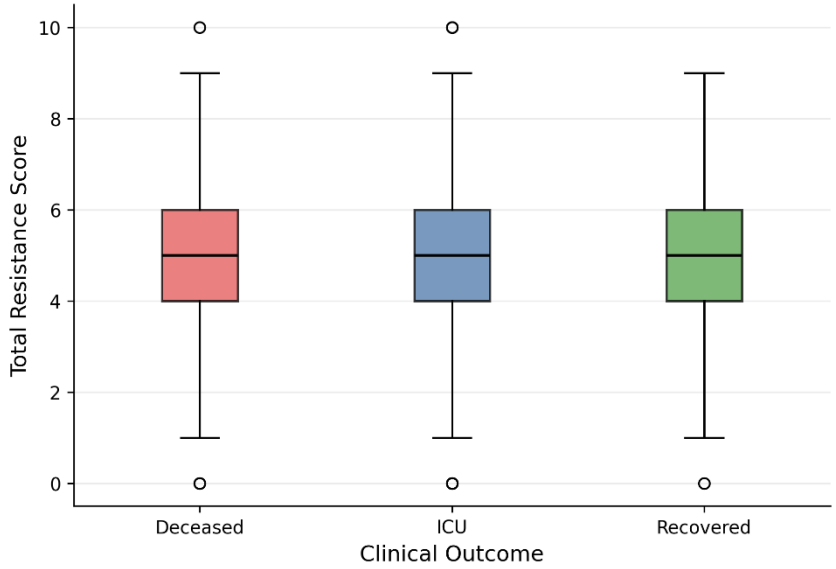

Figure 6. Resistance burden across clinical outcomes

3.6 Logistic Regression Analysis of Mortality Predictors

A binary logistic regression model was used to test for the association between demographic factors and mortality, as well as AMR-related factors (Table 7). Age (OR = 0.9995, p = 0.764), being male (OR = 0.9204, p = 0.368), being MDR (OR = 1.0394, p = 0.798), and total resistance score (OR = 0.9738, p = 0.429) did not reveal any statistical significance when tested against mortality.

Table 7. Logistic regression analysis for mortality predictors

Variable	Coefficient	Odds Ratio	P-value
Constant	-0.6034	0.5470	0.000828
Age	-0.0005	0.9995	0.764021
Gender Male	-0.0830	0.9204	0.367911
MDR Binary	0.0387	1.0394	0.798034
Total Resistance Score	-0.0265	0.9738	0.428731

3.7 Correlation Analysis of Study Variables

The correlation analysis revealed a moderately high correlation coefficient (r = 0.655) between the MDR status and the total resistance score (Figure 7). However, the correlations between all other parameters of demographics, mortality, and resistance markers were very low and nearly zero, suggesting almost negligible linear association between those factors (Table 8). As seen from Figure 8, the total resistance score was distributed mostly in the moderate range, and the maximum concentration of isolates occurred in the resistance score equal to 5.

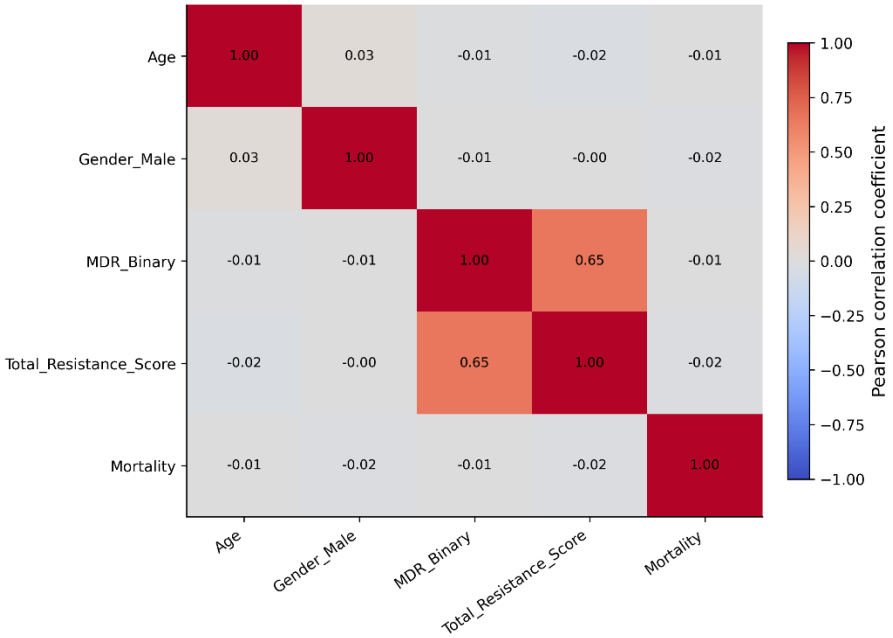

Figure 7. Correlation matrix

Table 8. Correlation matrix of study variables

Variable	Age	Gender Male	MDR Binary	Total Resistance Score	Mortality
Age	1.000	0.025	-0.009	-0.024	-0.006
Gender (Male)	0.025	1.000	-0.007	-0.001	-0.019
MDR Binary	-0.009	-0.007	1.000	0.655	-0.007
Total Resistance Score	-0.024	-0.001	0.655	1.000	-0.017
Mortality	-0.006	-0.019	-0.007	-0.017	1.000

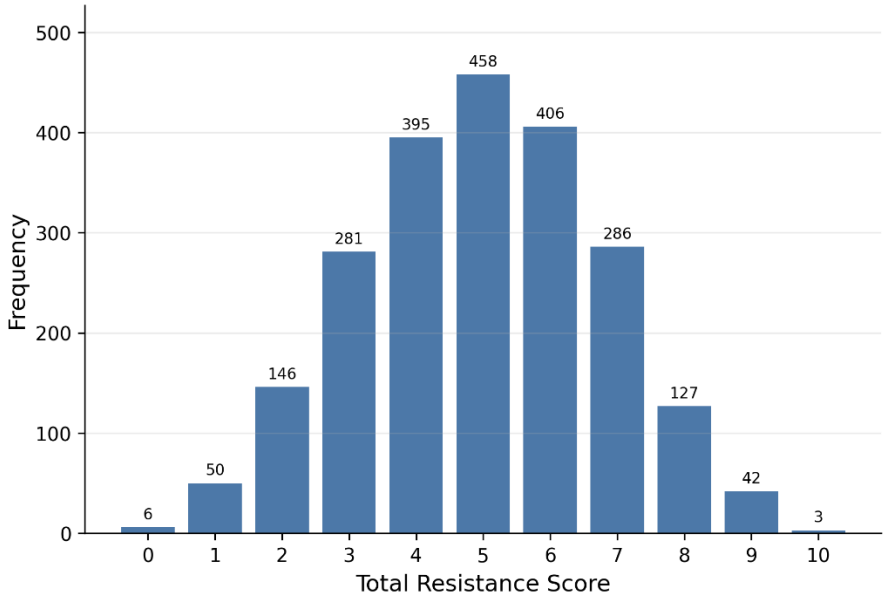

Figure 8. Distribution of total resistance scores

4. Discussion

From the analysis, there exists an AMR burden in clinical bacterial isolates, with 20.55% of the samples having multidrug resistance. Despite the fact that non-MDR made up the larger proportion, it is noteworthy that 1-in-5 had MDR due to the fact that MDR could affect treatment options. As such, it can be seen that resistance was distributed across several antibacterial agents since the numbers were relatively similar in all five antibiotics tested. The highest percentage of resistance was observed with respect to meropenem, which might show concerns for carbapenem resistance in this cohort. This is of significance considering the fact that carbapenems are generally known to have efficacy in treating severe bacterial infections. On the contrary, colistin had the highest percentage of sensitivity, thus retaining activity. However, the fact that resistant samples exist to the reserve medication means that caution is still necessary since they are used in cases where others are ineffective. Resistance gene distributions showed that VIM was the most common gene detected, followed by OXA-48. Meanwhile, KPC and NDM-1 genes were equally distributed. This implies a relatively even distribution of the different markers of resistance, meaning that they were not dominated by a particular resistance gene. Nevertheless, it was observed that MDR status was not associated with the resistance category, specimen type, gender, test type, or clinical outcome. Similarly, resistance burden was not significantly different for deceased patients, ICU and recovery patients. Further, logistic regression revealed that neither age, male gender, MDR status, nor total resistance scores significantly predicted mortality. From this, it can be deduced that there might be many other variables responsible for mortality, such as pathogen virulence, comorbidities, immunostatus, antibiotic timing, infection severity and source control. Moderately high positive correlation between MDR status and total resistance score reflects the validity of the scoring approach. MDR isolates were expected to show higher cumulative resistance burden. However, low correlations between resistance burden indicators and mortality imply that resistance burden alone cannot predict clinical outcome variability.

The observed prevalence of MDR infections aligns with the understanding that infections with such bacteria are a serious problem, especially if they lead to sepsis. Kumar et al. (2024) pointed out that MDR sepsis is a difficult condition to treat because late administration of proper treatment may deteriorate prognosis and make the treatment more complicated. The observation of genes associated with carbapenemase production (NDM-1, VIM, KPC and OXA-48) shows agreement with surveillance results, which state that these enzymes could be present in clinically significant bacterial isolates. For example, Flores et al. (2020) stated that NDM-producing Klebsiella pneumoniae were found together with VIM, KPC and OXA-48 enzymes during surveillance of intensive care units' culture samples. High resistance rate to meropenem is consistent with concerns about carbapenem resistance among hospital populations. Moghnieh et al. (2021) found carbapenem resistance among inpatients colonized or infected with 3rd-generation cephalosporin-resistant Enterobacterales and pointed to the potential value of risk assessment in predicting carbapenem resistance.

The relatively high sensitivity rate of colistin in the current investigation is consistent with its status as a last-resort therapeutic agent in the treatment of severe gram-negative infections despite the fact that it is highly toxic and develops resistance (El-Sayed Ahmed et al., 2020). Variable susceptibility rates across various antibiotics coincide with tertiary care findings showing that resistance rates vary depending on pathogen, specimen and local antibiotic usage. For example, Handa et al. (2024) described heterogeneity in antibiotic resistance rates for clinical bacterial pathogens. Lack of association between ICU outcomes and MDR status in the current dataset might partially be explained by its isolate-level nature. Environmental and transmission dynamics in the ICU play a role in the persistence and spread of MDR bacteria, as was shown by D'Souza et al. (2019) with spatiotemporal dynamics of MDR bacteria in ICU environments. Non-significant association of mortality with resistance burden differs from findings in disease-specific studies that link resistant infections with poor prognosis. Gao et al. (2024) provided the characteristics and dynamics of transmission of multidrug-resistant or rifampicin-resistant tuberculosis.

Further analysis might benefit from advanced surveillance techniques. For example, Forde et al. (2023) highlighted the value of routinely conducted whole genome sequencing for infection control of multidrug-resistant pathogens. The current findings correspond to the clinical burden described in multi-hospital surveillance. For instance, Lin et al. (2020) described the increasing prevalence of MDR isolates in 66 hospitals in the USA. Additionally, Gandra et al. (2019) pointed to the mortality burden caused by MDR pathogens in India.

As seen, AMR surveillance should continue to ensure optimal antimicrobial stewardship and appropriate treatment decisions. MDR infection prevalence indicates that resistance surveillance is needed. Resistance scoring might be useful for summarizing overall resistance burden in clinical isolates. However, outcome prediction must take into account not only AMR information, but also pathogen identity, antibiotic use history, infection severity and comorbidities.

It is worthwhile to note that there are a few limitations in this study. First of all, this work utilized secondary data and, therefore, was limited to the available variables only. Organism identity, comorbidity, antibiotic treatment history and infection severity were not known. In future studies, those variables could be used.

5. Conclusion

The burden of antimicrobial resistance was found in the isolated clinical strains since there was the presence of MDR in 20.55% of patients' specimens. Meropenem exhibited the highest level of resistance, whereas colistin had the maximum rate of sensitivity. This demonstrated the variability of the efficacy of different antibiotics against bacteria in this study. The resistance genes included those of VIM, OXA-48, KPC, and NDM-1. MDR was not statistically significantly associated with gender, specimen type, testing technique, resistance genes, or clinical result. Likewise, the resistance score was not statistically significantly higher in recovered, ICU, and dead individuals. There was no difference in the

mortality odds of those with various ages, genders, MDR and resistance burden based on logistic regression analysis. The moderate association of MDR with resistance burden indicated the usefulness of total resistance scoring as an aggregate index. The results of this study confirmed the importance of AMR surveillance and susceptibility testing, as well as the interpretation of resistance scores within the context of clinical factors. Further research involving the identification of pathogens, antibiotic treatments, and other clinical details is required.

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