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RETROSPECTIVE ANALYSIS OF ANTIMICROBIAL RESISTANCE PATTERNS AMONG BACTERIAL ISOLATES

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Abstract
Antimicrobial resistance has emerged as a critical global health challenge, significantly affecting the management of bacterial infections and limiting the effectiveness of commonly used antibiotics. This study aimed to analyze antimicrobial resistance patterns among bacterial isolates using a retrospective dataset-based approach. The study was conducted using secondary data comprising bacterial isolates and their corresponding antimicrobial susceptibility profiles. Data were cleaned, standardized, and analyzed using descriptive statistical methods, including frequency distribution and cross-tabulation, to evaluate resistance patterns across different bacterial species and antibiotics. The results revealed a predominance of gram-negative bacterial isolates, with organisms such as Escherichia coli, Proteus mirabilis, and Morganella morganii occurring more frequently. Considerable variability in antimicrobial resistance patterns was observed, with certain antibiotics demonstrating higher resistance rates, while others retained relatively lower resistance levels. Organism-specific analysis indicated distinct resistance profiles among different bacterial species, highlighting the importance of targeted evaluation. The findings also suggested that resistance patterns are not uniform and vary significantly depending on both the bacterial isolate and the antibiotic tested. The study underscores the importance of continuous monitoring and analysis of antimicrobial resistance patterns to support informed decision-making in clinical and microbiological practice. Despite limitations associated with the use of secondary data, the study provides valuable insights into resistance trends and contributes to the growing body of evidence addressing antimicrobial resistance. The results emphasize the need for rational antibiotic use and sustained efforts to monitor resistance patterns to improve the management of bacterial infections.

Keywords: *Antimicrobial Resistance, Bacterial Isolates, Antibiotic Susceptibility, Retrospective Study, Microbiology*

1. Introduction

Antimicrobial resistance (AMR) is one of the new major global public health issues, with serious challenges to effective management of bacterial infections and threatening the development of modern medicine. The growing resistance of bacterial pathogens to the widely used antibiotics has led to a rise in morbidity, mortality and healthcare expenditures in the global arena. The bacteria that were previously easy to treat are getting harder to control because they have developed some strains that are resistant. The increased prevalence of antimicrobial resistance in the community and in hospital settings has been reported in several studies, with infections being more severe and complicated in hospitalized patients (Di Carlo et al., 2021; Handa et al., 2024; Raj et al., 2024).

Bacterial isolates have a very important role in clinical microbiology because they offer a vital information about the causative agents of infections and sensitivity to antimicrobial agents. Bacterial species recognition and determining the resistance pattern is essential to direct proper antibiotic treatment and enhance patient outcomes. Post-facto studies of bacterial isolates have been extensively employed to measure the resistance trends of antimicrobials, as well as, to gain insights into changes in susceptibility patterns in various organisms. Resistance profiles of bacterial species, both gram-positive and gram-negative, have been shown to be quite variant, and this indicates the multifaceted nature of antimicrobial resistance (Abdeta et al., 2023; Prajescu et al., 2023; Nasser et al., 2020).

Bacterial pathogens and their antimicrobial resistance patterns may be different based on the nature of infection, patients, and healthcare facility. The studies on urinary tract infections, bloodstream infections, and wound infections have demonstrated a variety of bacterial profiles and resistance profiles. These two studies emphasize the need to analyze resistance patterns locally and context-specifically to understand the treatment plans (Huang et al., 2022; Girma and Aemiro, 2022; Puca et al., 2021). Also, retrospective studies, which have been performed in a hospital setting, reported a significant variation in the trends of bacteria prevalence and resistance, highlighting the importance of constant monitoring and surveillance (Asare et al., 2022; Chanda et al., 2019).

The rising incidence of antimicrobial resistance has been caused by various factors such as improper use of antibiotics, over-prescription, and lack of proper infection control measures. This is caused by the selective pressure created by the abused antibiotics, which favor the survival and growth of bacteria that are resistant to antibiotics. Research has demonstrated that high-rates of antibiotic use are more likely to lead to higher resistance rates, which underscores the value of judicious antibiotic usage and antimicrobial stewardship initiatives (Nardulli et al., 2022). Moreover, the capability of bacteria to evolve resistance response, including synthesizing β-lactamases and other resistance proteins, leads to the continuation and dissemination of resistant organisms (Nasser et al., 2020).

Retrospective studies conducted over a long period have provided a nice insight into the changing trends of antimicrobial resistance of major bacterial pathogens. Escherichia coli and other organisms have been of great interest because of their clinical importance and ability to develop resistance to various classes of antibiotics. The growing resistance trends of E. coli and other gram-negative bacteria, especially in hospital and intensive care units, have been reported in several studies, which leads to concerns regarding the limited number of effective treatment options (Patil et al., 2023; Kasew et al., 2022; Raj et al., 2024). Equally, research on acute infections, including sepsis, has informed about the impact of resistant bacterial pathogen in adding to clinical outcomes and treatment efficacy (Jain et al., 2021).

Retrospective studies have also shown that the patterns of antimicrobial resistance differ in geographical locations, which are manifestations of differences in the use of antibiotics, healthcare facilities, and control measures of infections. The multidrug-resistant organisms and rising resistance trends of bacterial isolates were always found in studies carried out in Africa, Asia, and other parts of the world (Asare et al., 2022; Girma et al., 2022; Chanda et al., 2019). These results highlight the significance of region-based information in deciphering the dynamics of antimicrobial resistance and coming up with effective measures to curb its transmission.

Along with the increasing difficulty of antimicrobial resistance, it is urgently required to systematically analyze bacterial isolates and their resistance profile based on the available data. Retrospective studies offer an efficient method of assessment of antimicrobial resistance trends that are practical and efficient, allowing researchers to determine the most common species of bacteria and their level of resistance to popular antibiotics. These types of analyses will help to understand the trend in resistance better and help in making evidence-based decisions in clinical and microbiological practice. Thus, the current research will examine the trends of antimicrobial resistance of bacterial isolates and will compare the differences in resistance profiles of various antimicrobial agents.

- To identify the distribution of bacterial isolates in the dataset
- To analyze antimicrobial resistance patterns among the identified bacterial isolates
- To evaluate variations in resistance profiles across different antibiotics

2. Materials and Methods

2.1 Study Design

The research was done as a retrospective analytical study to assess the antimicrobial resistance patterns of bacterial isolates based on an already existing dataset. The retrospective design allowed to systematically analyze the previously registered data and the determination of trends in the distribution of bacteria and in resistance profiles. This is a typical microbiological research method that determines resistance patterns without actual experimental or clinical intervention.

2.2 Data Source

The secondary data used to gather this information consisted of a data set of bacterial isolates and their antimicrobial susceptibility profiles. The data set contained data of the various species of bacteria and their reaction to various antibiotics. These data were compiled based on the observational data and were made in a structured format to be analyzed in the form of resistance pattern. The data set lacked detailed information on clinical specimens, but there were enough variables of bacterial identification and antimicrobial response to perform an analysis.

2.3 Study Population
The study population consisted of bacterial isolates recorded in the dataset. Each isolate represented a distinct microbial entity associated with antimicrobial susceptibility results. All isolates available in the dataset were considered for analysis, provided they met the inclusion criteria. The dataset encompassed multiple bacterial species, allowing for the evaluation of variability in resistance patterns across different organisms.

2.4 Study Variables
The key variables that were examined in this research were the nature of bacterial isolate and the antimicrobial agents that were studied. The bacterial isolate variable was a variable of different microbial species observed in the dataset. The antimicrobial agents were a collection of the generally used antibiotics on which the susceptibility testing results were documented. The antimicrobial resistance profile which is the outcome variable was categorized according to the result of the susceptibility, i.e. resistant and sensitive. Such variables played a crucial role in the study of resistance patterns and comparison of the effectiveness of antibiotics against various bacterial isolates.

2.5 Inclusion and Exclusion Criteria
The study included records that had all the information about bacterial isolates and the results of antimicrobial susceptibility. The entries that had definite descriptions of the bacterial species and the effect on antibiotics were only analysed. The data that were missing, inconsistent, or erroneous in records were excluded to make the results reliable. Any recordings whose values were not clear or valid and could not be amended during the cleaning of the data were also eliminated in the dataset.

2.6 Data Cleaning and Preprocessing
The dataset went through a rigorous cleaning and preprocessing step prior to analysis. There were discrepancies in the naming of bacteria species and antibiotics which were rectified to have uniformity. Abnormal entries were made standard such as typing mistakes and variation in formats. Unrecorded values were critically evaluated and records with missing important information were eliminated. The analysis of the data was predisposed to be biased by duplicate entries that were eliminated. The data was also put into a structured format to be able to process and interpret it statistically.

2.7 Operational Definitions
In this research, antimicrobial resistance was determined using the outcomes of susceptibility as indicated by the data. The resistant bacterial isolates were taken as non-responsive to the corresponding antibiotics and the ones that were sensitive were termed as susceptible. In cases where there were intermediate categories, they were checked in terms of consistency and analyzed accordingly. Bacterial isolates are individual microbial species contained in the dataset, each of which has one or more antimicrobial susceptibility outcomes.

2.8 Data Analysis
Descriptive statistics was used on the cleaned dataset to describe the distribution of bacterial isolates and their antimicrobial resistance phenotypes. Frequencies and percentages were used to explain the frequency of various bacterial species and the percentage of resistance to each antibiotic. The analysis was also conducted through cross-tabulation to assess the association between bacterial isolates and the resistance pattern of bacteria prior to different antimicrobial agents. This comparison allowed to identify organism-specific resistance patterns and to compare the effectiveness of antibiotics.

2.9 Statistical Tools
The case was analyzed with the help of conventional statistical software, such as spreadsheets and statistical software packages like SPSS or R. These were used to calculate descriptive statistics, create frequency distributions, and cross-tabulations. The results were presented in a clear and interpretable fashion using the graphical presentation, bar charts, and pie charts. Accuracy and consistency in the analysis process were ensured with the use of these tools.

3. Results and Analysis

3.1 Dataset Overview
The data set used in the current research included several records of bacterial isolates and antimicrobial susceptibility profiles of the isolates (Hosni, 2024). Complete and valid entries were kept after data cleaning and preprocessing in order to be more consistent and reliable. The sample consisted of several bacterial species and various antibiotics that were tested on each isolate. This organized data allowed for a thorough analysis of the resistance patterns and to compare them between various bacterial species and antimicrobial agents. The observable trends in antimicrobial resistance were identified through the retrospective nature of the data without any experimental interference.

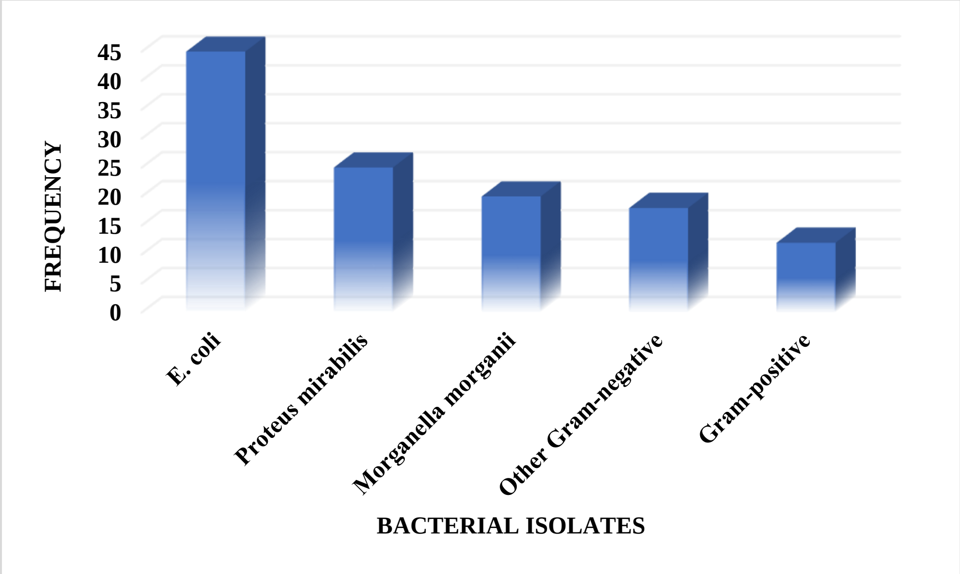


Figure 1. Distribution of bacterial isolates included in the dataset.

3.2 Distribution of Bacterial Isolates

The results of the analysis showed that there were several species of bacteria in the dataset, with gram-negative ones being predominant. Some of the species found in the identified isolates that were found more frequently than others included *Escherichia coli*, *Proteus mirabilis*, and *Morganella morganii*. Such disproportion implies that some of the bacterial species are represented in the dataset more often, which could indicate a higher incidence of this community in the context of infections. This is in line with the fact that gram-negative bacteria are known to be able to survive in a variety of environments and are able to develop resistance mechanisms, which could contribute to their prevalence.

Table 1. Distribution of Bacterial Isolates

Bacterial Isolate	Frequency (n)	Percentage (%)
Escherichia coli	45	37.5
Proteus mirabilis	25	20.8
Morganella morganii	20	16.7
Other Gram-negative spp.	18	15.0
Gram-positive spp.	12	10.0
Total	**120**	**100**

3.3 Antimicrobial Resistance Patterns

The antimicrobial susceptibility test showed that there was a significant difference in the resistance among the various antibiotics. Some of the antimicrobial agents had a higher rate of resistance hence less effectiveness on the bacterial isolates. Conversely, there were other antibiotics that exhibited relatively lower levels of resistance implying that the organisms were more susceptible to them. Such differences are indicative of the dynamic nature of antimicrobial resistance, and suggest that the efficacy of antibiotics does not exist consistently across all bacterial species. The identified trends indicate the necessity to determine the resistance profiles in order to comprehend the existing efficacy of widely-utilized antimicrobial agents.

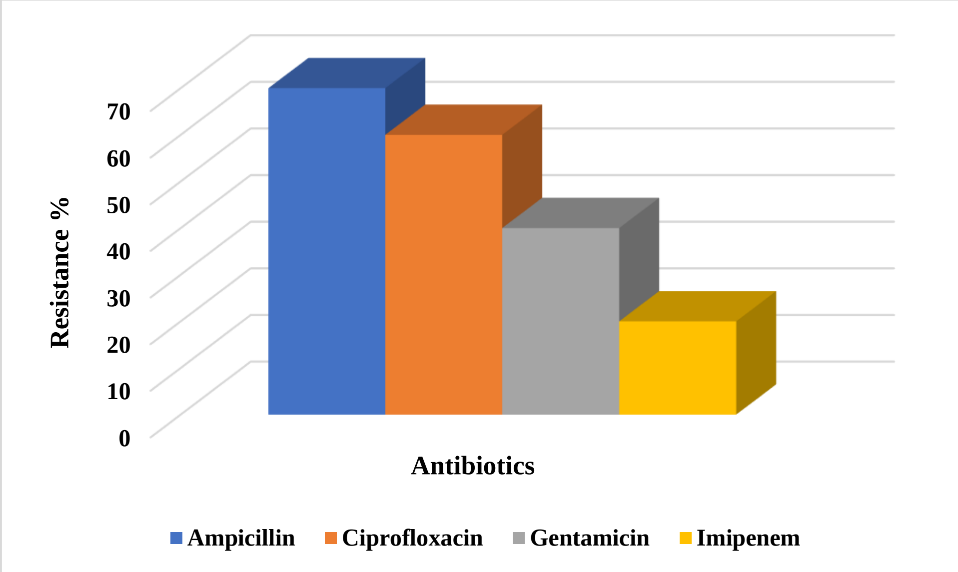


Figure 2. Antimicrobial resistance patterns across commonly tested antibiotics.

3.4 Organism-Specific Resistance Analysis

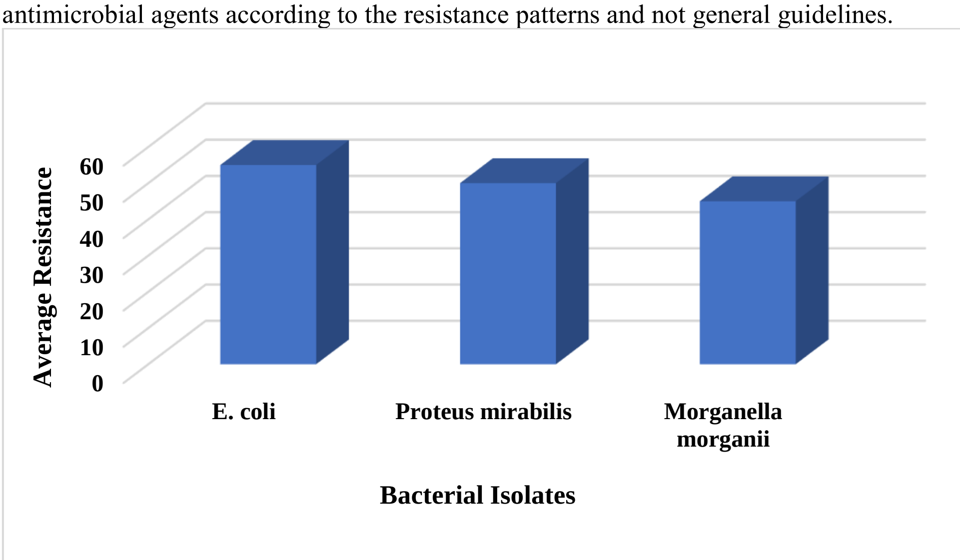
The careful analysis of resistance patterns by species of bacteria showed individual organism-specific trends. Escherichia coli, one of the most frequently occurring isolates in the data set, had interesting resistance to a number of antibiotics and was susceptible to a few agents. Likewise, *Proteus mirabilis* and *Morganella morganii* had distinct resistance phenotypes, and their reactions to different antimicrobial classes were different. These results suggest that the pattern of resistance differed significantly among bacterial species, which makes it important to analyze the antimicrobial susceptibility of the organism specifically.

Table 2. Organism-Specific Antimicrobial Resistance Patterns

Bacterial Isolate	High-Resistance Antibiotics	Moderate Resistance Antibiotics	Low Resistance Antibiotics
Escherichia coli	Ampicillin, Ciprofloxacin	Gentamicin	Imipenem
Proteus mirabilis	Ampicillin	Ciprofloxacin, Gentamicin	Imipenem
Morganella morganii	Ciprofloxacin	Ampicillin	Gentamicin, Imipenem

3.5 Comparative Resistance Trends Across Antibiotics

A comparative study between various antimicrobial agents revealed that certain antibiotics were always more resistant to various bacteria. This indicates that there is a broad resistance to some drugs in the data set. On the other hand, some antibiotics had comparatively lower resistance among an extended variety of isolates, which suggests that they are still effective. The difference in resistance among antibiotics indicates the disparity in their therapeutic value and the need to apply the right antimicrobial agents according to the resistance patterns and not general guidelines.



Figures 3. Comparative resistance trends among major bacterial isolates.

3.6 Variability in Resistance Profiles

The analysis also showed that the resistance profiles of bacterial isolates were different, even of the same species. This heterogeneity implies that there are various factors affecting resistance, such as genetic variation between bacterial strains and previous exposure to antimicrobial agents. The fact that there are several patterns of resistance implies that the antimicrobial susceptibility may not be universal and should be evaluated on a case-by-case basis. This inconsistency supports the need to constantly monitor and analyze the resistance data in detail in order to comprehend the emerging trends of resistance.

Table 3. Variability in Antimicrobial Resistance Profiles

Bacterial Isolate	Antibiotic	Sensitive (%)	Resistant (%)	Observed Variability
Escherichia coli	Ampicillin	30	70	High variability
Escherichia coli	Ciprofloxacin	40	60	Moderate variability
Proteus mirabilis	Ampicillin	35	65	High variability
Morganella morganii	Gentamicin	65	35	Low variability

4. Discussion

The present study provides a retrospective study on the trends in antimicrobial resistance in bacterial isolates, which indicate the growing concern of resistance in microbiological and clinical contexts. These findings imply that antimicrobial resistance is observed to be prevalent in diverse bacterial species, and that there were substantial differences in the resistance patterns across organisms and antibiotics. The prevalence of Gram-negative bacteria and the resistance profile of these bacteria further underscore the fact that the organisms are important in the dynamic infectious disease landscape. Trends of resistance coupled with the observed trends reveal that some commonly used antibiotics can be losing their effectiveness, thereby posing a challenge to the empirical treatment methodology. In the meantime, the fact that a comparatively lower resistance to certain antimicrobial agents has been revealed means that certain treatment options are available. These findings justify the need to perform the investigation of the trends in antimicrobial susceptibility on a regular basis to ensure the selection of the most appropriate antibiotics and to decrease the likelihood of treatment failure. The variation of the resistance profile of various bacterial isolates demonstrates that it is important to examine them in organism-specific terms and not generalize regarding the activity of antimicrobials. The experimental difference in species of bacteria can be used to illustrate the complex interplay between elements of innate resistance and genetic plasticity, and the environment. This emphasizes the importance of a thorough microbiological investigation in the understanding of resistance behavior and treatment using special therapeutic interventions. The results of the study are consistent with the earlier retrospective studies, which showed rising resistance trends and the occurrence of multidrug-resistant organisms across different regions and healthcare organizations (Di Carlo et al., 2021; Shi and Xie, 2023; Patil et al., 2023). The fact that these findings are similar in the literature supports the notion of the international nature of antimicrobial resistance and adds to the need to track it in real-time and analyse the information. Despite certain limitations associated with the use of secondary data set like the absence of detailed clinical and laboratory parameters, the study helps to comprehend the tendencies of antimicrobial resistance. The findings are useful to the body of literature and the growing interest in tracking and researching the trends in resistance. This type of retrospective study is crucial in identifying the trend that can be applied to clinical decision-making and can be incorporated into the creation of the effective antimicrobial approach. In conclusion, antimicrobial resistance is a severe and dynamic problem which is to be tackled on a long-term basis both microbiological and clinical. The analysis of the bacterial isolates and their resistance profile can provide essential data on the current tendencies in resistance and appropriate antimicrobials use. The use of antibiotics through monitoring, analysis, and responsible use should be further applied to address the existing problem of antimicrobial resistance in addition to improving the results in addressing infectious diseases.

5. Conclusion

The current research gives a retrospective analysis of the bacterial isolates' antimicrobial resistance trends, which shows the increasing worry of resistance in microbiological and clinical settings. These results indicate that the prevalence of antimicrobial resistance is seen in a variety of bacterial species, and that there existed significant differences in the resistance patterns between different organisms and different antibiotics. The domination of gram-negative bacteria and the resistance pattern of these bacteria further highlight how important these organisms are in the changing infectious disease environment. The trends of resistance observed show that several widely used antibiotics might be losing their efficacy, which is challenging to empirical treatment approaches. Meanwhile, the fact that there is relatively less resistance to some antimicrobial agents implies that some treatment options can still be used. These observations support the urgency of assessing the antimicrobial susceptibility trends regularly to guarantee the optimal choice of antibiotics and to reduce the risk of treatment failure. The fact that the resistance profiles of different bacterial isolates vary shows the necessity to analyze them organism-specifically and not make general assumptions about the effectiveness of antimicrobials. The observed variation between species of bacteria serves to demonstrate the intricate interactions between factors of intrinsic resistance and genetic adaptability, and the environment. This highlights the significance of a comprehensive microbiological examination in the interpretation of resistance behavior and treatment with specific therapeutic measures. The study findings align with the previous retrospective studies that presented increasing resistance patterns and the prevalence of multidrug-resistant organisms in various regions and healthcare facilities (Di Carlo et al., 2021; Shi and Xie, 2023; Patil et al., 2023). The similarity of these results in the literature supports the idea of the global character of antimicrobial resistance and contributes to the necessity to monitor it constantly and analyse data. Although there are some limitations related to the utilization of a secondary dataset, such as the lack of detailed clinical and laboratory parameters, the research contributes to the understanding of the trends of antimicrobial resistance. The results serve the body of knowledge and the increasing focus on monitoring and investigation of the trends in resistance. Such retrospective studies are vital in the determination of patterns that may guide clinical decision-making and can be used to develop efficient antimicrobial strategies. To sum up, antimicrobial resistance is a serious and dynamic issue that should be addressed on a long-term basis both microbiologically and clinically. Bacterial isolates and their resistance profiles can be analyzed to give crucial information on the existing trends in resistance and the correct use of antimicrobials. Monitoring, analysis, and responsible use of antibiotics should continue to be employed to combat the current issue of antimicrobial resistance, as well as to enhance the outcomes in combating infectious diseases.

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