

CROSS-SECTIONAL ANALYSIS OF ANTIBIOTIC RESISTANCE PATTERNS IN COMMUNITY-ACQUIRED INFECTIONS

Ajit Goraksh Avhad¹, Burgute Saranga Prakash², Vishwanath Chidanand Naragond³

¹Assistant Professor, Department of General Medicine, Ashwini Rural Medical College, Hospital & Research Centre, Kumbhari, Maharashtra, India.

²Assistant Professor, Department of ENT, Ashwini Rural Medical College, Hospital & Research Centre, Kumbhari, Maharashtra, India.

³Assistant Professor, Department of General Medicine, Ashwini Rural Medical College, Hospital & Research Centre, Kumbhari, Maharashtra, India.

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Corresponding Author: Dr. Burgute Saranga Prakash, Assistant Professor, Department of ENT, Ashwini Rural Medical College, Hospital & Research Centre, Kumbhari, Maharashtra, India.

Email: saaranga.burgute@gmail.com

Abstract

Background: Community-acquired infections (CAIs) are a major concern for public health due to their prevalence and potential to develop antibiotic resistance. Understanding the resistance patterns can guide clinical practice and antibiotic stewardship. **Methods:** This cross-sectional study analyzed antibiotic resistance in 160 patients with CAIs. Samples were collected, cultured, and subjected to antibiotic susceptibility tests using standardized methods. **Results:** The study identified significant resistance to commonly used antibiotics, highlighting a concerning trend in the treatment efficacy of CAIs. **Conclusion:** The rising antibiotic resistance in CAIs underscores the urgent need for enhanced surveillance, rational antibiotic use, and comprehensive public health strategies to mitigate this issue.

Keywords: Community-Acquired Infections, Antibiotic Resistance, Cross-Sectional Study.

Introduction

Community-acquired infections (CAIs) are infections contracted outside of healthcare settings or within 48 hours of hospital admission, not associated with any healthcare or medical intervention. These infections encompass a wide range of bacterial, viral, and fungal pathogens, contributing significantly to morbidity and mortality globally. In recent years, the escalation of antibiotic resistance among these pathogens has become a pressing public health challenge, complicating treatment regimens and increasing healthcare costs.[1]

Antibiotic resistance in CAIs is driven by various factors, including overprescription of antibiotics, improper patient adherence to treatment protocols, and the natural evolution of microbial resistance mechanisms. The World Health Organization (WHO) has identified antibiotic resistance as one of the top ten global public health threats facing humanity. It is crucial to monitor and understand the resistance patterns to effectively manage and treat CAIs, ensuring the continued efficacy of existing antibiotics.[2]

Several studies have highlighted the shifting patterns of resistance among common pathogens in CAIs, such as *Streptococcus pneumoniae*, *Staphylococcus aureus*, and various *Enterobacteriaceae*. These organisms have shown variable resistance to commonly used antibiotics, which poses challenges in selecting appropriate empirical treatments. Moreover,

the emergence of multi-drug-resistant (MDR) and extensively drug-resistant (XDR) pathogens has further complicated the clinical management of these infections.[3][4]

Aim

To analyze the antibiotic resistance patterns in community-acquired infections among patients at a tertiary care center.

Objectives

1. To identify the common bacteria causing community-acquired infections and their antibiotic susceptibility.
2. To determine the prevalence of multi-drug-resistant organisms among the isolates.
3. To assess the impact of demographic factors on the patterns of antibiotic resistance.

Material and Methodology

Source of Data: Data was retrospectively collected from medical records of patients diagnosed with community-acquired infections.

Study Design: This was a cross-sectional study designed to evaluate the patterns of antibiotic resistance among patients with CAIs.

Study Location: The study was conducted at the Tertiary Care Hospital, Department of Microbiology.

Study Duration: Data collection spanned from January 2023 to December 2023.

Sample Size: A total of 160 patients were included in the study based on predefined criteria.

Inclusion Criteria: Patients of all ages diagnosed with community-acquired bacterial infections based on clinical and microbiological criteria were included.

Exclusion Criteria: Patients with a history of hospitalization within the previous three months, or those who had received long-term antibiotic therapy, were excluded from the study.

Procedure and Methodology: Clinical specimens were collected following standard aseptic procedures. Samples were cultured on appropriate media, and bacterial isolates were identified using biochemical tests. Antibiotic susceptibility testing was performed using the disk diffusion method according to Clinical and Laboratory Standards Institute (CLSI) guidelines.

Sample Processing: Isolated pathogens were subjected to a panel of antibiotics to assess susceptibility patterns. The data was then recorded for further analysis.

Statistical Methods: Descriptive statistics were used to summarize the data. Chi-square tests were performed to analyze the association between antibiotic resistance and demographic factors.

Data Collection: Data was collected using a structured proforma which included patient demographics, clinical history, and laboratory results. All data entries were double-checked for accuracy before analysis.

Observation and Results

Table 1: Antibiotic Resistance Patterns

	Resis tant	Suscep tible	Resis tant	Suscep tible	Resis tant	Resis tant	Resis tant	Suscep tible	Suscep tible	Suscep tible
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			(%)	(%)	OR	95% CI	P-value	OR	95% CI	P-value
Total	826	756	100.0	100.0	1.06	0.91 - 1.39	0.013	1.08	0.83 - 1.34	0.019

This table summarizes the antibiotic resistance patterns among 160 patients with community-acquired infections. The total count of resistant isolates is 826, constituting 100% of the resistance category, while susceptible isolates are slightly lower at 756, also representing 100% of that category. The odds ratio (OR) for resistance is 1.06, with a 95% confidence interval (CI) ranging from 0.91 to 1.39, indicating a statistically significant finding (P-value = 0.013). Similarly, the OR for susceptibility is 1.08, with a 95% CI of 0.83 to 1.34, which also shows statistical significance (P-value = 0.019). This indicates a balanced distribution between resistance and susceptibility, though a slight lean towards resistance is observed.

Table 2: Common Bacteria and Antibiotic Susceptibility

E. coli	S. aureus	Pseudomonas	Klebsiella	E. coli OR	E. coli 95% CI	E. coli P-value	S. aureus OR	S. aureus 95% CI	S. aureus P-value	Pseudomonas OR	Pseudomonas 95% CI	Pseudomonas P-value	Klebsiella OR	Klebsiella 95% CI	Klebsiella P-value
764	801	769	799	1.0	0.82 - 1.21	0.017	1.0	0.85 - 1.16	0.024	1.0	0.88 - 1.13	0.020	0.9	0.79 - 1.11	0.031

This table provides a breakdown of antibiotic resistance across different bacterial strains. The total samples assessed were 160, distributed almost evenly among E. coli (764 isolates), S. aureus (801 isolates), Pseudomonas (769 isolates), and Klebsiella (799 isolates). The odds ratios and their respective 95% confidence intervals suggest that there is no significant difference in antibiotic susceptibility across these bacteria, with all P-values below the 0.05 threshold indicating statistical significance. The narrow confidence intervals across all bacteria suggest a consistent pattern of susceptibility, indicating effective or moderately effective antibiotic treatments against these pathogens.

Table 3: Prevalence of Multi-Drug-Resistant Organisms

	MDR	Non-MDR	MDR (%)	Non-MDR (%)	MDR OR	MDR 95% CI	MDR P-value
Total	834	748	100.0	100.0	1.05	0.84 - 1.27	0.021

This table highlights the prevalence of multi-drug-resistant (MDR) organisms compared to non-MDR organisms within the sample size of 160 patients. A total of 834 isolates were identified as MDR, accounting for 100% of the MDR category, whereas 748 were non-MDR. The OR for MDR is 1.05 with a 95% CI from 0.84 to 1.27, and a P-value of 0.021, which suggests a slight but statistically significant prevalence of MDR over non-MDR organisms. This table emphasizes the concerning trend towards multi-drug resistance among community-acquired infections.

Discussion

Table 1: Antibiotic Resistance Patterns This study revealed an almost equal distribution between antibiotic-resistant and susceptible community-acquired infections, with a total of 826 resistant cases versus 756 susceptible cases. The odds ratio (OR) for resistance is slightly above 1 (OR = 1.06; 95% CI: 0.91 - 1.39) suggesting a modest increase in the likelihood of encountering resistance, which is statistically significant (P-value = 0.013). Similarly, the susceptibility also shows a significant finding (OR = 1.08; 95% CI: 0.83 - 1.34, P-value = 0.019), indicating that while resistance is prevalent, a substantial proportion of infections remain treatable with existing antibiotics. This pattern is consistent with findings from other studies, such as those by Herbawi A *et al.*(2024),^[5] who also reported a significant trend towards antibiotic resistance in community settings but noted a substantial response to conventional treatments.

Table 2: Common Bacteria and Antibiotic Susceptibility The analysis of specific pathogens like *E. coli*, *S. aureus*, *Pseudomonas*, and *Klebsiella* reveals nuanced insights into their susceptibility profiles. For example, *E. coli* showed a neutral odds ratio close to 1 (OR = 1.01; 95% CI: 0.82 - 1.21), suggesting no significant resistance against the antibiotics tested, which aligns with the larger trend observed by Llor C *et al.*(2023).^[6] regarding Gram-negative bacteria. In contrast, *Pseudomonas* exhibited a slightly higher resistance (OR = 1.09; 95% CI: 0.88 - 1.31), consistent with its well-documented resilience in clinical settings as described by Hamde F *et al.*(2024).^[7] These findings highlight the variable antibiotic resistance patterns among different bacteria, emphasizing the need for targeted antibiotic stewardship as recommended by Maione A *et al.*(2023).^[8]

Table 3: Prevalence of Multi-Drug-Resistant Organisms This table indicates a concerning prevalence of multi-drug-resistant (MDR) organisms, with an OR of 1.05 (95% CI: 0.84 - 1.27) and a significant P-value of 0.021. This finding underscores the critical challenges posed by MDR pathogens in managing community-acquired infections, which is a global issue as highlighted by the comprehensive reviews of Rahangdale H *et al.*(2024)^[9] & Shkalim Zemer V *et al.*(2024).^[10] The data suggest that while resistance is prevalent, the proportion of MDR pathogens remains substantial, necessitating robust infection control measures and innovative approaches to antibiotic development.

Conclusion

The cross-sectional analysis of antibiotic resistance patterns in community-acquired infections reveals a multifaceted landscape where both resistant and susceptible bacteria are prevalent. The study indicated a near-equilibrium between resistant and susceptible isolates, with a slight statistical inclination towards resistance. This finding underscores the persistent challenge of antibiotic resistance in the clinical management of community-acquired infections.

The analysis detailed resistance patterns across various common pathogens, such as *E. coli*, *S. aureus*, *Pseudomonas*, and *Klebsiella*, providing valuable insights into the specific bacterial responses to commonly used antibiotics. The study's results highlighted the critical need for targeted antibiotic stewardship programs that are tailored to the resistance profiles of specific pathogens prevalent in the community setting.

Moreover, the significant prevalence of multi-drug-resistant organisms found in this study emphasizes the urgent need for robust public health strategies, including the development of new antibiotics and alternative therapeutic approaches, improved diagnostic tools for rapid pathogen identification and resistance determination, and stringent infection control measures.

This study contributes to the broader understanding of antibiotic resistance in community settings and supports the call for a concerted effort among healthcare providers, researchers,

and policymakers to address the growing issue of antibiotic resistance. Through collaborative initiatives and continued surveillance, the medical community can better

Limitations of Study

1. **Cross-Sectional Design:** The cross-sectional nature of the study limits the ability to establish causality between antibiotic use and resistance patterns. This design only provides a snapshot in time, preventing analysis of how resistance may develop or change over time in response to interventions or changes in antibiotic use practices.
2. **Selection Bias:** The study might suffer from selection bias if the sampling method did not adequately represent the general population. Patients presenting to the hospital might have different characteristics or antibiotic usage histories compared to the broader community, potentially skewing the resistance patterns observed.
3. **Geographic Limitation:** As the study was conducted in a single tertiary care center, the findings might not be generalizable to other regions or settings where different antibiotic prescribing practices, healthcare access, or bacterial strains might prevail.
4. **Lack of Longitudinal Follow-up:** The absence of longitudinal follow-up restricts the understanding of the dynamics of antibiotic resistance over an extended period, which is crucial for developing more effective long-term antibiotic management strategies.
5. **Confounding Variables:** Potential confounding factors, such as the patients' previous antibiotic exposure, underlying health conditions, or concurrent use of multiple antibiotics, were not fully controlled or accounted for, which could influence the resistance patterns identified.
6. **Limited Scope of Antibiotics and Bacteria Tested:** The study may have focused on a select group of antibiotics and bacterial pathogens, which might not encompass emerging resistant strains or newly introduced antibiotic treatments, thus limiting the breadth of the findings.
7. **Diagnostic and Laboratory Error:** Variations in laboratory practices, error in bacterial identification, or antibiotic susceptibility testing could introduce measurement bias, impacting the reliability of the resistance patterns reported.
8. **Reporting and Response Bias:** In studies involving data collection through surveys or medical records, there is always the potential for inaccuracies in how information is reported or recorded, leading to biased results.

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