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Comparative Analysis of Antibiotic Resistance Patterns before and After the Covid-19 Pandemic

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ABSTRACT

Antimicrobial resistance (AMR) is a major global public health challenge that has been further influenced by changes in antibiotic usage during the COVID-19 pandemic. The present study evaluated and compared antibiotic resistance patterns among bacterial isolates obtained from human clinical samples during pre-COVID and post-COVID periods. A total of 120 clinical specimens, including urine, sputum, pus, wound swabs, blood, and throat swabs, were processed using standard microbiological methods. Out of these, 92 samples showed significant bacterial growth. Antibiotic susceptibility testing was performed using the Kirby–Bauer disc diffusion method following CLSI guidelines.

The results demonstrated increased resistance during the post-COVID period, particularly among Gram-negative pathogens such as *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Acinetobacter baumannii*. A significant increase in antimicrobial resistance was observed during the post-COVID period, particularly among Gram-negative pathogens.

High resistance was detected against ampicillin and amoxicillin, whereas gentamicin retained comparatively better activity. The findings highlight the impact of excessive antibiotic usage during the pandemic and emphasize the need for antimicrobial stewardship and rational antibiotic prescribing.

Keywords: Antibiotic Resistance, Antimicrobial Resistance, COVID-19, Multidrug Resistance, Antibiotic Susceptibility, Antimicrobial Stewardship

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INTRODUCTION

Antibiotics represent one of the most important advances in modern medicine and have significantly reduced morbidity and mortality caused by bacterial infections. Since the discovery of penicillin by Alexander Fleming, antimicrobial agents have transformed healthcare and improved outcomes in surgery, transplantation, intensive care medicine, and infectious disease management. However, excessive and irrational use of antibiotics has accelerated the emergence of antimicrobial resistance (AMR), which is now recognized as one of the greatest threats to global public health.

Antimicrobial resistance occurs when microorganisms develop the ability to survive exposure to drugs that were previously effective against them. Resistant infections result in prolonged illness, increased healthcare expenditure, treatment failure, and mortality. The emergence of multidrug-resistant organisms such as Methicillin-resistant *Staphylococcus aureus* (MRSA), carbapenem-resistant *Klebsiella pneumoniae*, and multidrug-resistant *Pseudomonas aeruginosa* has complicated infection management worldwide.

The COVID-19 pandemic substantially altered antibiotic prescription practices. Although COVID-19 is caused by SARS-CoV-2, a viral pathogen, antibiotics were extensively prescribed because of concerns regarding secondary bacterial infections. Empirical administration of broad-spectrum antibiotics became common in hospitalized patients despite relatively low rates of confirmed bacterial co-infections. This excessive antibiotic consumption may have accelerated the emergence and spread of resistant bacterial strains.

The present study was undertaken to evaluate antibiotic resistance patterns among bacterial isolates obtained during pre-COVID and post-COVID periods and to assess the impact of pandemic-associated antibiotic usage on antimicrobial resistance trends.

MATERIALS AND METHODS

The study was designed as a laboratory-based observational and comparative investigation conducted to evaluate antibiotic resistance patterns among bacterial isolates recovered from human clinical samples collected during pre-COVID and post-COVID periods. Retrospective data were obtained from archived laboratory records representing the pre-COVID era, whereas prospective analyses were performed on clinical specimens collected during the post-COVID period.

Clinical specimens included urine, sputum, pus, wound swabs, blood, and throat swabs collected from patients attending outpatient departments, inpatient wards, emergency units, and intensive care units. Samples were collected aseptically and transported to the microbiology laboratory in sterile containers for immediate processing.

Gram staining was performed for preliminary classification of bacterial isolates. Culture was carried out on Nutrient Agar, MacConkey Agar, and Blood Agar, followed by incubation at 37°C for 18–24 hours. Identification of bacterial isolates was achieved through colony morphology, Gram staining characteristics, and biochemical tests including Indole, Methyl Red, Voges–Proskauer, Citrate Utilization, Catalase, Coagulase, and Oxidase tests.

Antibiotic susceptibility testing was performed using the Kirby–Bauer disc diffusion method on Mueller–Hinton Agar according to Clinical and Laboratory Standards Institute (CLSI) guidelines. A standardized inoculum equivalent to 0.5 McFarland standard was prepared before testing. Antibiotics evaluated included amoxicillin, ampicillin, ciprofloxacin, ceftriaxone, cefixime, gentamicin, tetracycline, and azithromycin. Results were interpreted as sensitive, intermediate, or resistant according to CLSI criteria.

RESULTS AND DISCUSSION

3.1 Distribution of Clinical Samples

A total of 120 clinical specimens were included in the study. Urine samples constituted the largest proportion, followed by pus/wound swabs and sputum samples.

Table 1. Distribution of Clinical Samples

Sample Type	Number	Percentage (%)
Urine	45	37.5
Pus/Wound Swab	30	25.0
Sputum	25	20.8
Blood	10	8.3
Throat Swab	10	8.3
Total	120	100

The predominance of urine samples reflects the high prevalence of urinary tract infections among patients attending healthcare facilities.

3.2 Culture Positivity Rate

Out of 120 specimens processed, 92 demonstrated significant bacterial growth, whereas 28 showed no growth or contamination.

Table 2. Culture Positivity Rate

Result	Number	Percentage (%)
Positive Growth	92	76.6
No Growth/Contaminated	28	23.4
Total	120	100

The high culture positivity rate indicates a substantial burden of bacterial infections within the study population.

3.3 Distribution of Gram-Positive and Gram-Negative Isolates

Gram-negative bacteria predominated among the recovered isolates.

Table 3. Gram Staining Characteristics of Isolates

Type	Number of Isolates	Percentage (%)
Gram-Positive	35	38
Gram-Negative	57	62
Total	92	100

The predominance of Gram-negative bacteria is clinically significant because these organisms are frequently associated with multidrug resistance and healthcare-associated infections.

3.4 Distribution of Bacterial Isolates

Identification of bacterial isolates demonstrated that Escherichia coli was the most common pathogen, followed by Staphylococcus aureus and Klebsiella pneumoniae.

Table 4. Distribution of Bacterial Isolates

Bacterial Isolate	Number	Percentage (%)
Escherichia coli	30	32.6
Staphylococcus aureus	22	23.9
Klebsiella pneumoniae	15	16.3
Pseudomonas aeruginosa	10	10.8
Proteus spp.	8	8.6
Acinetobacter baumannii	7	7.6
Total	92	100

3.5 Comparative Analysis of Pre-COVID and Post-COVID Resistance Trends

Comparison between pre-COVID and post-COVID periods demonstrated a noticeable increase in resistant bacterial isolates following the pandemic.

Table 5. Comparative Distribution of Selected Resistant Isolates

Organism	Pre-COVID	Post-COVID
Klebsiella pneumoniae	6	9
Acinetobacter baumannii	2	5

The increase in resistant isolates during the post-COVID period supports concerns regarding the impact of widespread empirical antibiotic usage during the pandemic.

3.6 Antibiotic Susceptibility Pattern

Antibiotic susceptibility testing revealed substantial resistance against several commonly prescribed antibiotics.

Table 6. Overall Antibiotic Susceptibility Pattern

Antibiotic	Sensitive (%)	Resistant (%)
Amoxicillin	28	72
Ampicillin	25	75
Ciprofloxacin	48	52
Ceftriaxone	40	60
Cefixime	35	65
Gentamicin	62	38
Tetracycline	45	55
Azithromycin	38	62

Ampicillin exhibited the highest resistance rate, followed by amoxicillin, cefixime, and azithromycin. Gentamicin demonstrated the highest sensitivity and remained comparatively effective against several bacterial pathogens.

3.7 Impact of COVID-19 on Antimicrobial Resistance

The increased resistance observed during the post-COVID period may be attributed to extensive empirical antibiotic therapy, prolonged hospitalization, increased intensive care admissions, and disruption of antimicrobial stewardship programs during the pandemic. Similar findings have been reported globally, indicating a growing burden of multidrug-resistant bacterial infections following COVID-19.

The findings of the present study highlight the need for rational antibiotic prescribing, routine culture and susceptibility testing, antimicrobial stewardship programs, and continuous surveillance to prevent further escalation of antimicrobial resistance.

CONCLUSION

The present study demonstrated a significant increase in antimicrobial resistance among bacterial isolates during the post-COVID period compared to the pre-COVID era. Gram-negative bacteria were the predominant pathogens isolated, with *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Acinetobacter baumannii* representing the major organisms associated with resistant infections. Antibiotic susceptibility testing revealed high resistance against ampicillin, amoxicillin, cefixime, and azithromycin, while gentamicin exhibited comparatively better effectiveness.

The findings suggest that excessive antibiotic consumption during the COVID-19 pandemic may have accelerated the emergence of resistant bacterial strains and multidrug-resistant organisms. Rational antibiotic prescribing, antimicrobial stewardship programs, routine culture and susceptibility testing, infection control measures, and public awareness initiatives are essential to combat the growing threat of antimicrobial resistance. Preservation of antibiotic effectiveness remains critical for ensuring successful treatment of infectious diseases and protecting global public health.

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