Demographic Profile and Bacterial Spectrum of Respiratory Tract Infections: A Laboratory-Based Study of Culture-Positive Isolates

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Abstract- Respiratory infections among bacteria have continued to be a major cause of morbidity in hospitals especially with the rising number of antimicrobial resistance. The current investigative project was carried out to examine the demographic profile and distribution of respiratory pathogenic bacteria based on laboratory-confirmed information. There were 191 culture-positive respiratory isolates in the study. Out of these 115 (60.2%) of the isolates were male patients and 76 (39.8%) were female patients. The distribution in terms of age indicated that the greatest percentage of cases was recorded in the 61-80 years' age bracket (47.6%), then 41-60 years (23.6%) and 21-40 years (19.9) thus showing that older individuals are more susceptible to the disease. Microbiological identification showed that *Pseudomonas aeruginosa* (30.9%) was the most commonly isolated organism followed by *Escherichia coli* (25.1%), *Staphylococcus aureus* (18.3%), and *Klebsiella pneumoniae* (17.8%). Others were *Acinetobacter baumannii* (4.2%), Enterococcus spp. (1.6%), *Streptococcus pyogenes* (1.0%), and *Streptococcus pneumoniae* (1.0%). The results show the prevalence of Gram-negative microorganisms and the increased burden of infection in the elderly patients. To manage the situation with respiratory infections in the clinics, it is necessary to implement continuous monitoring of the distribution and patterns of antimicrobial resistance, as well as rational use of antibiotics.

Keywords: Respiratory infections, bacterial pathogens, demographic profile, culture-positive isolates, antimicrobial-resistance

I.INTRODUCTION

Respiratory tract infections (RTIs) are one of the most pressing global public health issues remaining the cause of a high level of morbidity and mortality, in particular, in hospitalized and immunocompromised patients (GBD Lower Respiratory Infections Collaborators, 2022; World Health Organization, 2023). These infections have a broad clinical spectrum, including mild infections of the upper respiratory tract, or serious infections of the lower respiratory tract, including pneumonia and acute respiratory syndrome disorder (ARDS) (Torres et al., 2021). The clinical consequences of RTIs are also made complex by the fact that they are attributed to longer hospitalization, high health care expenditures, and complications. Bacterial pathogens are very important in both the community-acquired and hospital-acquired respiratory infections. These infections are linked to poor clinical outcomes in most instances, especially patients who are critically ill and those patients who are under intensive care support (Timsit et al., 2020). Bacterial respiratory infections are multifactorial with their epidemiology being determined by various factors, such as host characteristics, environmental exposures, and healthcare practices. Age and sex are considered to be some of the host-related factors of susceptibility and progression of the disease. Elderly people are especially susceptible because of immunosenescence, which causes progressive deterioration of the immune system and limits the body in its ability to effectively fight infections (Nikolich-Žugich, 2018). It is also contributed to by a decrease in mucociliary clearance, physiological reserves, and comorbidities, including diabetes mellitus, chronic obstructive pulmonary disease (COPD), and cardiovascular disorders (World Health Organization, 2023). On the contrary, younger people are usually less susceptible with rather stable immunological reactions and less underlying health issues. Inequalities in the occurrence of respiratory infections in gender have also been reported in a wide manner. Such disparities can be explained by different levels of environmental exposure, risk in the workplace, smoking, and healthcare use (Timsit et al., 2020). Moreover, social economic and behavioural issues can supplement the distribution of the disease and access to healthcare among the populations.

Antimicrobial resistance (AMR) of respiratory pathogens is a serious issue becoming an international concern in recent years. The growing rates of multidrug-resistant (MDR) organisms have considerably reduced the shortening of therapeutic decisions and made it more difficult to treat respiratory infections (Dadgostar, 2019; World Health Organization, 2023). The gram-negative bacteria, especially the *Pseudomonas aeruginosa* and *Klebsiella pneumoniae* have shown a significant rise in resistance to most commonly used antibiotics, including carbapenems, which are usually regarded as the last-resort antibiotics (World Health Organization, 2023).

The hospital setting has a major role in the emergence and spread of resistant organisms. Selective antibiotic pressure, extended hospitalization, invasive device usage, and poor infection control practices are some of the factors that lead to the development of resistant strains (Timsit et al., 2020). These issues also indicate that it is critical to monitor the spread of pathogens and trends of antimicrobial susceptibility on a regular basis to implement effective empirical treatment and to sustain antimicrobial stewardship interventions (Torres et al., 2021).

As bacterial profiles and resistance patterns are dynamic, the data about the region are necessary to make a sound clinical decision. Local epidemiology research offers highly useful information on the existing pathogens and their resistance mechanisms, allowing clinicians to maximize treatment regimens and achieve better patient outcomes. Thus, the current research has been conducted to assess the demographic profile and the spectrum of bacteria of culture-positive respiratory tract infections according to the laboratory information. The results are expected to add to the local epidemiological data and help create specific interventions that will help manage respiratory infections more efficiently (World Health Organization, 2023; Timsit et al., 2020).

II.METHODOLOGY

Study Design and Setting

This was a retrospective, lab-based study that was carried out in the Department of Microbiology in one of the tertiary care hospitals in the Delhi NCR area within a specified period of study (October, 2024 to March, 2025).

Study Population and Sample size

The total respiratory specimen that was received in the microbiology lab was 460. Out of these 191 samples which showed a high level of bacteria growth were further evaluated. The study only took culture-positive isolates, and excluded culture-negative and contaminated samples.

Sample Collection

In this research, respiratory samples, including sputum samples, throat swabs, endotracheal (ET) samples, and bronchoalveolar lavage (BAL) samples were used. The patients provided their sputum samples in leak-proof containers that were sterilized with proper guidance to have quality samples. Sterile swabs dipped in normal saline were used to collect throat swabs. Clinicians used standard aseptic procedures in the collection of ET aspirates and BAL samples during routine procedures. The specimens were prepared well and taken to the microbiology laboratory at the earliest time possible to avoid delays in processing (World Health Organization, 2019).

Microbiological Processing

Microbiological tests were used to open and process the respiratory samples in order to achieve optimal bacterial pathogen recovery. The samples were inoculated on the right culture media and incubated under controlled environmental conditions. Aseptic practices were followed to the letter in order to prevent contamination and provide reliability of findings (Forbes et al., 2021).

Identification and Antimicrobial susceptibility testing

Isolates of bacteria were characterized according to morphology of colonies, Gram staining, and a combination of the biochemical reactions. Also, automated identification systems were used where necessary to enhance the accuracy of diagnosis and decrease the turnaround time (Murray et al., 2020). Antimicrobial susceptibility testing was done by the VITEK 2 Compact system automated (bioMerieux, France) according to the protocol of the manufacturer. The system offers fast and standardized identification of the pattern of susceptibility to a large number of antimicrobial agents. The interpretation of results was done according to the Clinical and Laboratory Standards Institute guidelines (Clinical and Laboratory Standards Institute, 2023; BioMérieux, 2021).

III.STATISTICAL ANALYSIS

All the information was organized and analyzed with Microsoft Excel. Descriptive statistics techniques were used and the findings were stated in frequencies and percentages that are easy and significant to interpret (Daniel et al., 2019 ; Field, 2018).

Formula used

1. Frequency (n): The number of occurrences of a particular variable (e.g., number of isolates, number of sensitive/resistant cases) (Mongomery et al., 2014).
2. Age wise distribution (%): (Daniel et al., 2019)
   Age group percentage= Number of cases in age group ×100
   Total no. of cases
3. Organism wise distribution (%):(World health organization, 2018)
   Organism percentage= Number of isolate of specific organism ×100
   Total isolates

IV.RESULT

The present study used a total number of 191 culture-positive respiratory isolates (100%). Out of them, 115 isolates (60.2%) were found as male and 76 isolates (39.8%) were found as female, which means that the infections were more widespread among males (Table 1& figure 1). Analysis of ages demonstrated that most of the cases fell within the 61-80 years' age group comprising 47.6% (n = 91) out of all the isolates. This was then furthered by the 41–60 years' age group (23.6%, n = 45) and the 21-40 years' age group (19.9% n =38). The percentage of cases was lower in patients older than 80 years (6.3% n = 12) and 0-20 years old (2.6% n = 5), which means that the prevalence of infections was lower among younger patients (Figure 2). The distribution of bacterial pathogens showed the preponderance of Gram-negative ones. *Pseudomonas aeruginosa* was the most commonly isolated pathogen with a rate of 30.9% (n = 59) of all the isolates. This was succeeded by *Escherichia coli* (25.1% n = 48), *Staphylococcus aureus* (18.3% n = 35) and *Klebsiella pneumoniae* (17.8% n = 34). The other organisms that were less frequently isolated were *Acinetobacter baumannii* (4.2, n = 8), *Enterococcus faecalis* (1.6, n = 3), *Streptococcus pyogenes* (1.0, n = 2), and *Streptococcus pneumoniae* (1.0, n = 2) (Figure 3).

Performing antimicrobial susceptibility testing, by means of the VITEK 2 Compact system, it was observed that there was a worrying trend of resistance among the isolates. There was resistant evidence against the regularly used antibiotics especially cephalosporins and fluoroquinolones. *Pseudomonas aeruginosa* and *Klebsiella pneumoniae* were Gram-negative organisms that were found to be less susceptible to various classes of antimicrobials, including carbapenems in some instances. Nevertheless, agents of last-resort, including colistin, were found to be more sensitive. There was a significant percentage of isolates with multidrug-resistant (MDR) phenotypes, which demonstrates the increasing difficulty of the successful treatment of respiratory infections. Age-related trends in antimicrobial response are evident in the table 2. While middle-aged patients (41–60 years) show moderate sensitivity with mixed organism patterns, younger adults (21–40 years) show higher sensitivity with effective response to medications like Linezolid and Colistin. On the other hand, older patients (>60 years) exhibit significantly lower sensitivity and greater resistance, especially in *K. pneumoniae* and *E. coli*, suggesting a higher prevalence of multidrug-resistant infections (Table 3). In general, it can be concluded that Gram-negative bacteria were more common among older ones, whereas The gram-positive organisms were relatively more distributed across the age groups but there were higher percentages of older patients.

Table 1: Gender-wise distribution of positive patients

Gender	Number	Percentages
Male	115	60.20%
Female	76	39.80%
Total	191	100%

Table 2: - Age-wise Distribution of Bacteria

Organism	0-20 years	21-40 years	41-60 years	>60 years
E. col (n=48)	0 %	18.75 %	20.83 %	60.42 %
K. pneumoniae (n=34)	2.94 %	11.76 %	23.53 %	61.76 %
P. aeruginosa (n=59)	3.33 %	23.33 %	25 %	48.33 %
A. baumannii (n=8)	0%	25%	12.5%	62.5%
S. aureus (n=35)	5.88 %	23.53 %	29.41 %	41.18 %
S. pneumoniae (n=2)	0%	50%	0%	50%
S. pyogenes (n=2)	0%	100%	0%	0%
E. faecalis (n=3)	0%	33.33%	33.33%	33.33%

Table 3: - Age-wise Antibiotic sensitivity pattern

Age group (years)	Predominant organism	Sensitivity pattern	Resistant Antibiotics	Sensitive Antibiotics
0-20	E.coli, K.pneumoniae, S.aureus	High Sensitivity	Low Resistance	Colistin, Tigecycline, Carbapenems, Amikacin
21-40	*S. aures, P. aeruginosa*	High Sensitivity	Low Resistance	Linezolid, Colistin, Tigecycline, Amikacin
41-60	Mixed organisms	Moderate	Moderate	Aminoglycosides, Carbapenems
>60	*E.coli, K. pneumoniae, A. baumannii*	Low Sensitivity	High resistance	Colistin, Tigecycline

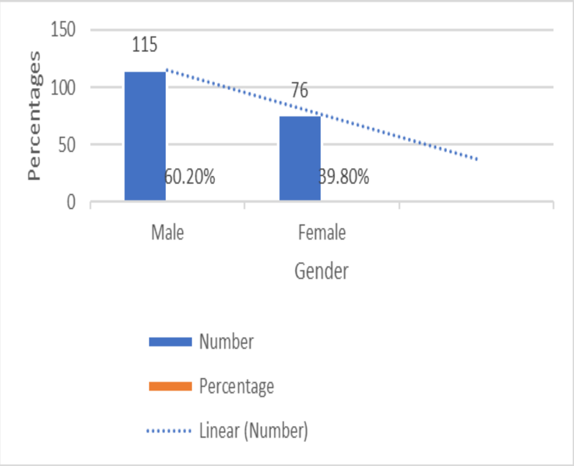

Figure 1: - Gender Distribution

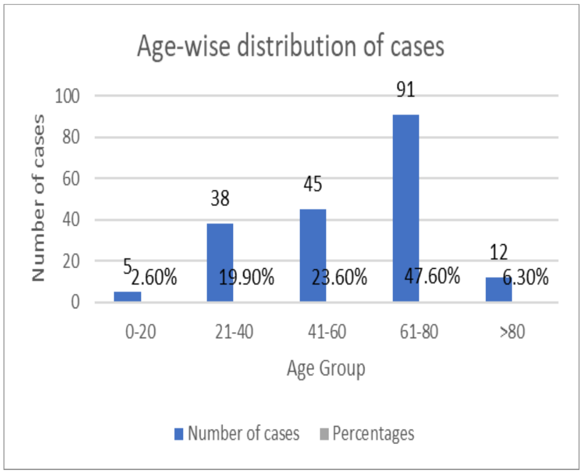

Figure 2: - Age-wise Distribution

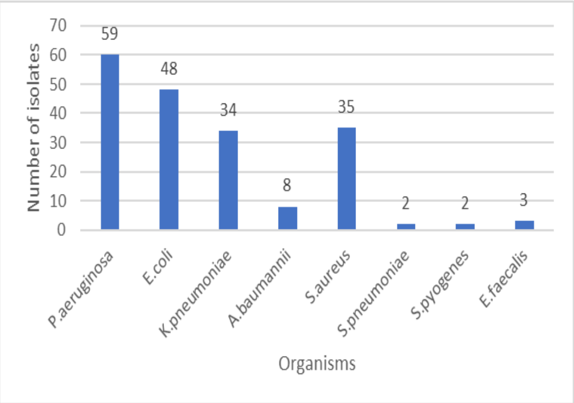

Figure 3: - Distribution of bacterial isolates

V.DISCUSSION

The current paper offers a thorough analysis of demographics, bacteria profile, and antimicrobial resistance trends of the culture-positive respiratory tract infections. The results bring to fore significant epidemiological and clinical patterns that play a significant role in informing empirical treatment and infection control measures. The rate of infection among male patients (60.2%) was higher as compared to female patients (39.8%). This sexual difference has been continuously mentioned in earlier findings and can be explained by the fact that males are more likely to be exposed to environmental pollutants, work-related risks, tobacco, and healthcare-seeking behavioural differences (Falagas et al., 2007; Torres et al., 2021). Also, the existence of sociocultural aspects and poor access to healthcare by some groups can also add to this difference. The analysis was based on age, and it was found that most infections affected the old people, especially within the age category of 61-80 years (47.6%). The observation is consistent with the previous studies that recognize advanced age as one of the key risk factors of respiratory infections. This higher vulnerability is attributable to the fact that older people are susceptible to immunosenescence, which is a progressive decrease in the immune system, a decrease in mucociliary clearance, and the presence of numerous comorbid diseases, including diabetes, chronic obstructive pulmonary disease (COPD), and cardiovascular diseases (Nikolich-Žugich, 2018; GBD Lower Respiratory Infections Collaborators, 2022). Moreover, their likelihood of having infections with resistant organisms could be due to the frequent hospitalization and exposure to antibiotics in their age group. Conversely, the somewhat lesser rates among the younger population indicate superior immune functioning and a reduced number of comorbidities.

Microbiological results of the current work have indicated that the Gram-negative bacteria were predominant, and *Pseudomonas aeruginosa* was the most frequently isolated pathogen. This follows the findings of various hospital-based studies that have identified *P. aeruginosa* and *Klebsiella pneumoniae* as the major causative agents of respiratory infections, especially in patients who are critically ill and ventilated (Timsit et al., 2020; Torres et al., 2021). Such high prevalence of *Escherichia coli* further indicates that opportunistic pathogens have an increasingly important role to play in immunocompromised and hospitalized patients. The role of nosocomial infections, which is usually linked to the extended length of stay in the hospital, admission to the intensive care unit (ICU) and invasive interventions like mechanical ventilation, is supported by the presence of *Acinetobacter* species and other non-fermenting Gram-negative bacilli. Even though Gram-negative organisms were the most dominant, Gram-positive bacteria with a significant contribution to the overall infection burden were also present, especially *Staphylococcus aureus*. This observation shows that community-acquired and hospital-acquired pathogens coexist in the respiratory tract infection. Their clinical significance and the necessity to consider Gram-positive organisms in the context of empirical treatment plans is further supported by the presence of such organisms in dissimilar age groups.

Another issue that is raised by this study is the fact that the level of antimicrobial resistance is high among the isolates. There was a high resistance to the widely used antibiotics like cephalosporins, fluoroquinolones, amoxicillin-clavulanic acid, and cotrimoxazole. The results are consistent with the reports provided worldwide, showing that the number of multidrug-resistant (MDR) organisms among respiratory pathogens is growing rapidly (World Health Organization, 2023; Dadgostar, 2019). The decreased susceptibility to carbapenems that are usually reserved as the last-line agents in the treatment of severe infections is of special concern and indicates the development of carbapenem-resistant organisms in the study setting.

The comparatively high sensitivity of the last-resort antibiotics, including colistin and tigecycline, provides few therapeutic alternatives, but they cannot be relied upon since they have toxicity profiles and resistance may develop. The rising prevalence of MDR phenotypes, particularly the gram negative bacteria indicate the dire nature of antimicrobial stewardship practices. Individualized prescription of antibiotics under the guidance of local antibiograms is necessary to reduce the exposure to unnecessary antibiotics and delay the resistance development.

The age-specific pattern of antibiotic response that was observed in the presented study further highlights the susceptibility of elderly populace where the highest levels of resistance and the prevalence of MDR had been registered. That can be explained by the accumulated exposure to antibiotics, a high number of hospitalizations, and comorbidities in elderly patients. Conversely, the patients who were younger had higher antimicrobial susceptibility profiles, which implied more positive clinical outcomes.

Clinically, this study has shown that the combination of microbiological data and patient-specific aspects in conducting effective treatment programs are critically important. Surveillance data that are specific to a region are important in guiding empirical therapy, especially in hospitals with high levels of antimicrobial resistance. Hand hygiene, environmental cleaning, and prudent use of invasive devices constitute part of infection prevention and control efforts and they are also vital in curbing the spread of resistant pathogens in healthcare environments.

To sum up, the current research exhibits the prevalence of Gram-negative pathogens, a growing tendency of antimicrobial resistance, and the predisposition of older people to respiratory tract infections. These results indicate the importance of vigilance and good antimicrobial stewardship behaviours and evidence-based clinical decisions to improve patient outcomes and combat the increasingly challenging problem of antimicrobial resistance.

VI.CONCLUSION

This paper has shown that Gram-negative bacteria were the leading cause of respiratory tract infections, with *Pseudomonas aeruginosa*, *Escherichia coli*, and *Klebsiella pneumonia* being the most prevalent isolates. The burden of infection among elderly patients (>60 years) was found to be higher and this shows that older patients are more susceptible to the infection. The patterns of antimicrobial susceptibility identified a strong resistance to the widely used antibiotics, especially cephalosporins, fluoroquinolones, and amoxicillin/clavulanic acid, whereas such drugs as linezolid, daptomycin, colistin, and tigecycline were more effective. The emergence of the methicillin-resistant *Staphylococcus aureus* (MRSA) also points to the increasing difficulty in the fight against antimicrobial resistance. It is worth noting that the resistance to antimicrobials was stronger in older patients (>60 years), which could be explained by the following factors: regular hospitalization, comorbidities, and previous use of antibiotics. All in all, it can be concluded that the important role of constant monitoring, rational administration of antibiotics, and strict infection control measures is necessary, in both high-risk elderly groups, because it will help to manage respiratory infections and reduce the propagation of resistant organisms.

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