INTRODUCTION

Community-acquired pneumonia (CAP) remains a common and serious illness despite the availability of potent new antimicrobials and effective vaccines. In the United States, pneumonia is the sixth leading cause of death from infectious diseases [1,2]. The mortality rate of pneumonia patients in outpatient settings is low, in the range of 1-5%, but among patients who require admissions to the intensive care unit, it approaches 25% [3-6]. The bacteriological profile of CAP patients is different in different countries and changing with time within the same country, probably due to frequent use of antibiotics, changes in environmental pollution, increased awareness of the disease, and changes in life expectancy. For example, Streptococcus pneumoniae remains the most common organism leading to CAP in most parts of Europe, the United States, the UK, and Iraq [7-10], whereas Klebsiella pneumoniae was the most common organism in a study from Singapore [11]. In India also, the bacteriological profile of pneumonia patients differs as per different geographic regions. This study was conducted to understand the bacteriological profile of pneumonia patients presenting to our tertiary care hospital in southern Rajasthan.

METHODS

This was a retrospective observational study conducted in a tertiary care hospital in southern Rajasthan. The duration of the study period was 6 months (June 2023–December 2023). All patients admitted with pneumonia were included in the study including patients admitted with CAP as well as patients who developed hospital-acquired pneumonia (HAP) and ventilator-associated pneumonia (VAP) at the time of admission to the hospital. All patients with diagnosis other than pneumonia were excluded from the study. The data were collected from medical records including sputum and bronchoalveolar lavage culture reports with antibiotic resistance patterns. Patients with no culture reports or negative culture reports were excluded from this study.

RESULTS

Fifty patients who were hospitalized with pneumonia were included in this study. The majority of patients were males (n=36, 72%), with an average age of 62 years. Patients admitted with CAP were 21, HAP were 15, and VAP were 14. The most common organism isolated was K. pneumoniae (n=18), followed by Acinetobacter baumannii (n=12), Pseudomonas aeruginosa (n=8), Escherichia coli (n=5), Staphylococcus aureus (n=2), methicillin-resistant Staphylococcus aureus (MRSA) (n=1), Burkholderia (n=1), COVID-19 (n=1), and swine flu H1N1 (n=2). Klebsiella was the most common organism isolated in patients with CAP (n=8) and also among HAP (n=5) and VAP (n=5) in our hospital (Fig. 1). Klebsiella isolated among HAP and VAP was more drug-resistant isolate as compared to the one isolated from community acquired pneumonia (CAP). The most of the patients who were having HAP/VAP had higher oxygen requirement and mortality rate as compared to CAP patients.

DISCUSSION

Out of 50 patients with pneumonia included in this study, 21 patients were of CAP, 15 patients had HAP, and 14 patients had VAP. Most of the patients were males and were of the elderly age group, with an average age of 62 years. Most of the patients had multiple comorbidities, the most common of which were smoking (55%), chronic obstructive pulmonary disease (COPD) (32%), hypertension (15%), and diabetes
In this study, K. pneumoniae (36%) was the most common organism isolated in sputum culture reports of CAP patients and also among HAP and VAP. Gram-negative bacteria were the most common organisms causing pneumonia in our study, followed by few cases of Gram-positive bacteria such as S. aureus and few viral causes such as COVID-19 and H1N1. This study highlights that in our region, Gram-negative bacteria play an important role in causing pneumonia even at a community level. A similar study conducted in Singapore also reported K. pneumoniae as the most common organism causing CAP [11]. It has been reported that old age, smoking, and COPD impair pulmonary defenses and predispose to CAP caused by Gram-negative bacteria [12,13]. Recent studies conducted in the last two decades have also shown a higher incidence of Gram-negative organisms causing culture-positive pneumonia [14-16]. Klebsiella was also the most common organism isolated in HAP as well as VAP, but it showed more antibiotic resistance as compared to CAP. Fig. 2 depicts a higher incidence of carbapenem-resistant Klebsiella in HAP and VAP as compared to CAP. A recent study conducted by Ramadan et al [17] and Bush [18] also showed a higher incidence of carbapenem resistance among K. pneumoniae isolates of HAP and VAP patients. Other organisms isolated were A. baumannii (24%), Pseudomonas (16%), E. coli (10%), S. aureus (9%), MRSA (2%), Burkholderia (2%), COVID-19 (2%), and swine flu (H1N1) (4%). Those bacteria which were carbapenem resistant on culture usually showed in vitro sensitivity to colistin, minocycline, and tigecycline on culture. We had a higher proportion of patients with HAP and VAP as our hospital being a tertiary referral center received more complicated pneumonia cases who had already been treated outside and not improving. This may be the reason for the higher percentage of resistant Klebsiella isolates found in our study.

CONCLUSION

This study showed that K. pneumoniae was the most common organism isolated in CAP as well as HAP and VAP patients. There is a rising incidence of Gram-negative bacteria causing CAP, especially in developing countries possibly due to the overuse of antibiotics which is alarming. Gram-negative organisms isolated from HAP and VAP showed higher carbapenem resistance.

Institutional Ethical Committee clearance was taken before starting this study.

CONFLICT OF INTEREST

Nil.

AUTHORS FUNDING

Nil.

REFERENCES


