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KEY WORDS: Ventilator associated pneumonia, nosocomial pneumonia, microbiological spectrum, aspiration.

STUDY OF MICROBIOLOGICAL SPECTRUM OF VENTILATOR ASSOCIATED PNEUMONIA

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ABSTRACT

Background: Ventilator associated pneumonia is one of the most common nosocomial infections caused by different bacterial species. A complete knowledge regarding the microbiological spectrum of VAP is needed to start empirical therapy as early as possible to prevent high morbidity and mortality. **Aims and Objectives:** To know the microbiological spectrum of ventilator associated pneumonia. **Materials And Methods:** Tracheal aspirates of 60 patients were collected and examined for different microbial species over a period of one year. **Results:** Out of 60 patients, Klebsiella (43.34%) was the commonest organism identified to cause VAP, followed by Pseudomonas (26.67%), Staphylococcus (20%), E.coli (6.67%) and Proteus (3.34%). **Conclusion:** Clinicians should have a clear understanding of the microbiological spectrum of VAP to start empirical therapy to avoid high mortality associated with VAP.

INTRODUCTION

Pneumonia, a common community acquired and hospital acquired infection, is called nosocomial pneumonia when it occurs in hospitalized patients. Nosocomial pneumonia is classified into healthcare associated pneumonia (HCAP), hospital acquired pneumonia (HAP) and ventilator associated pneumonia (VAP).[1] VAP is defined as pneumonia that is diagnosed after 48 hours of endotracheal intubation. Mechanical ventilation is the most important risk factor of VAP, and it occurs in 9 to 27% of intubated patients.[2] When compared with medical ICU cases, VAP is common in burns, surgical, trauma, neurological, and neurosurgical ICUs.[3] VAP risk increases with time required to hospitalise the patients and number of ventilator days. Large volume aspiration of aero-digestive tract organisms by ICU patients with altered immunity status is the major route of VAP. Patients with altered sensorium, altered gut motility and difficulty in swallowing are more prone to aspirate large volumes of fluid from aero digestive tract with virulent microorganisms. And, direct inhalation and hematogenous dissemination are less common.[1]

The main risk factors for VAP are aspiration due to supine position, nasogastric tube, enteral nutrition, decreased endotracheal tube cuff pressure, neuromuscular disease. coma, and surgery, COPD, prior antibiotic use, frequent ventilator circuit changes, and others such as severity of illness, ARDS, age > 60 years, and PRBC transfusion.[4] All patients on ventilators do not develop VAP. Some factors such as underlying disease of patients, geography, ICU population, duration of mechanical ventilation, prior antibiotic therapy, and method used to obtain respiratory culture influence the type of microorganism that is isolated.[1] Out of all of them, duration of mechanical ventilation, prior antimicrobial use, and local hospital infections determine the course and microbial spectrum of patients. Historically, the most prevalent organisms that have been causing nosocomial pneumonia are aerobic gram negative bacilli (58%).[5] The group of organisms that belong to the Enterobacteriaceae family are ubiquitous and require minimal nutrition, and hence, these are the common organisms that grow in many hostile environments. Other organisms that cause VAP are those that most commonly cause community acquired pneumonia such as *Streptococcus pneumoniae, Haemophilus influenzae,* and *Moraxella catarrhalis*. Other uncommon organisms are *Legionella*, anaerobic organisms, and fungi.[1]

Suspicion is raised when new or progressive radiologic infiltrates are found on chest X-ray associated with signs and symptoms of infection such as fever, leukocytosis, and purulent tracheal aspirate etc. Though traditionally difficult, diagnosis is by isolation of organisms from blood culture and culture of organisms in fluids obtained by bronchial-alveolar lavage or protected specimen brush or tracheal aspirate that are collected simultaneously.[6] However, even post-mortem histologic examination is also non-specific.[1]

MATERIALS AND METHODS:

The present study was conducted during the period of one year from July 2021 to June 2022 from different hospitals in Andhra Pradesh and Telangana state. A criteria was used to identify cases of VAP: fever, leukocytosis, purulent tracheal secretions, oxygen saturation, and chest radiographic findings. A total of 100 cases were selected initially by simple random sampling technique, but 40 patients were excluded finally because of lack of sufficient inclusion criteria. And finally, tracheal aspirates of 60 patients, who fulfilled inclusion criteria, were sent for further microbiological analysis. The tracheal isolates were examined initially using gram-staining technique, and then different media such as blood agar, chocolate agar, and MacConkey agar were used after incubation at 37 degrees Celsius for 48 hours. Then the VITEK 2 compact system and others were used to identify different isolates.

Type of Study: Cross sectional and observational study

Sampling Technique: Simple Random Sampling

Statistical Analysis

The data was entered into MS excel and analyzed using SPSS 2.0 software.

Eligibility Criteria

Inclusion Criteria:

Patients who were intubated and had new infiltrates in chest X-ray after 48 hours of intubation with other signs and symptoms such as fever, increased leukocyte count and purulent tracheal secretions.

Exclusion Criteria:

Patients who had prior infiltrates in chest X-ray and patients without fever, leukocytosis and tracheal aspirate without purulent secretions.

RESULTS:

In this study, a total of 60 patients with VAP are examined for causative organisms. Of 60 patients, 35 were males (58.34%) and 25 were females (41.67%). Patients were categorised based upon the number of days of ventilation also. Around 50

percent of patients are in the 10 to 20 days range. Only 5 patients (8.34%) are in the more than 20 days range. Of the 60 patients, *Klebsiella pneumoniae* is found in 26 patients (43.34%), *Pseudomonas* in 16 patients (26.67%), *Staphylococcus aureus* in 12 patients (20%), *Escherichia coli* in 4 patients (6.67%), and *Proteus* in 2 patients (3.34%).

Table 1 Showing Categorisation Of Number Of Patients According To Duration Of Ventilation And Gender.

Duration of ventilation	No. of patients	Males	Females
2-5 days	10 (16.67%)	6 (10%)	4 (6.67%)
6 to 10 days	15 (25%)	8 (13.34%)	7 (11.67%)
11 to 20 days	30 (50%)	18 (30%)	12 (20%)
> 20 days	5 (8.34%)	3 (5%)	2 (3.34%)
Total	60 (100%)	35 (58.34%)	25 (41.67%)

Table 2 Showing Percentage Of Organisms Isolated.

Type of organism isolated	Number of patients	Percentage
Klebsiella	26	43.34%
Pseudomonas	16	26.67%
Staphylococcus aureus	12	20%
Escherichia coli	4	6.67%
Proteus	2	3.34%
Total	60	100%

DISCUSSION:

Ventilator associated pneumonia is one of the commonest hospital acquired infections which increases the morbidity and mortality of patients. A complete knowledge and understanding of microbes is needed to rapidly start empirical therapy without waiting for aspirate culture reports, which is often delayed because of time required for bacterial growth. Hence, this study is conducted to know the microbiological spectrum of ventilator associated pneumonia so that empirical treatment can be started immediately after considering a diagnosis of VAP to prevent unnecessary morbidity and mortality. As described by Dr. William Osler, the founder of modern medicine, pneumonia is the "captain of the men of death", which occurs due to inflamed or infected alveoli.[7]

The overall incidence rate for VAP is around 10 to 70% according to a study conducted by Krishnamurthy et al.[8] In the present study, *Klebsiella* species were isolated in most of the cases, and it is followed by *Pseudomonas*, *Staphylococcus* and E.coli. However, in many studies, *Pseudomonas* was the leading organism in many cases (24%), but the trend has shifted in NHSN (January 2006 to October 2007) study with methicillin resistant staphylococcus aureus being at the top, followed by *Pseudomonas.*[9]

A study conducted by Maebed et al.[10], revealed gram negative organisms such as Klebsiella and Pseudomonas only, whereas in our study, staphylococcal species were also identified along with gram negative anaerobic organisms in 20% of patients, which is correlating relatively with NHSN study as described above, in which MRSA was found in more than 20 percent of cases.

Even in most of the studies such as Kanafani et al[11]. also revealed *Klebsiella* as the most common organism, which is correlating with our study. But, a study done in a Pakistani Clinic[12] revealed MRSA as the most common organism and *Klebsiella* was reported in less than 10 percent of cases. A study conducted by Rello et al[13]. showed that organisms that cause CAP were common in COPD patients and *S.aureus* was common in trauma and neurological patients.

However, in one study done in King Abdulaziz Medical City (KAMC) in Riyadh of Saudi Arabia reported *Acinetobacter* as the most common organism that caused VAP.[14] In our study, we could not find any species of *Acientobacter.* Even though extensive strategies are being employed to curtail the incidence of VAP, it still remains to be the main cause of death in patients with hospital acquired infections.[15]

CONCLUSION:

Ventilator associated Pneumonia is a most common nosocomial infection in mechanically ventilated ICU patients. It is a rapidly progressing complication with high morbidity and mortality, and hence, sufficient knowledge of microbiological spectrum is required to start empirical therapy immediately after collecting tracheal aspirate to prevent unnecessary further complications.

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