

# PATTERN OF BACTERIAL PATHOGENS ISOLATED FROM ENDOTRACHEAL SECRETIONS IN INTENSIVE CARE UNIT (ICU) PATIENTS OF A TERTIARY CARE HOSPITAL OF LAHORE

Muna Malik<sup>1</sup>, Muhammad Irfan Malik<sup>1</sup>, Ayesha Sajjad<sup>2</sup>

<sup>1</sup>Ameer ud din Medical College/ Post Graduate Medical Institute, Lahore General Hospital, Lahore Pakistan

<sup>2</sup>Amna Inayat Medical College, Lahore Pakistan

## ABSTRACT

**Objective:** To determine the frequency and pattern of bacterial pathogens in tracheal secretions of patients who developed VAP during their stay in Lahore General Hospital.

**Study design, Place and Duration of Study:** This descriptive study was carried out in Lahore General Hospital, Lahore during January to December 2017.

**Material and Methods:** Endotracheal secretions from 445 patients on ventilator support were included in the study. Patients with fever  $\geq 38^{\circ}\text{C}$ , WBCs count  $\geq 10,000/\text{mm}^3$  or  $\leq 3,000/\text{mm}^3$ , purulent tracheal secretions and diffuse or patchy infiltration in chest radiograph were included in the study. After Gram staining, the samples were inoculated on blood and MacConkey agar with crystal violet, and incubated up to 48 hours at  $37^{\circ}\text{C}$ . The isolates were identified by standard microbiological procedures in laboratory.

**Results:** Out of 445 samples of tracheal secretions, 365 were collected from males and 80 from females. 370 samples (83%) yielded growth on culture. Of these, 75 (20.3%) were polymicrobial. The commonest isolate was *Klebsiella pneumoniae*. Other isolates included *Pseudomonas aeruginosa*, *Acinetobacter spp.*, *E. coli*, *Proteus spp.* among Gram-negative bacteria and *Staphylococcus aureus* among Gram-positive bacteria.

**Conclusion:** Gram-negative bacilli are the commonest pathogens isolated from the endotracheal secretions of patients with ventilator-associated pneumonia.

**Key Words:** Tracheal secretions, ICUs, Ventilator associated pneumonia, Nosocomial infections.

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## INTRODUCTION

Intensive care units (ICUs) are specialized wards, which provide strict monitoring and special care to sick patients. Unfortunately, these specialized units are also more prone to hospital-acquired infections (HAIs). ICU patients have 5-7 times higher risk of acquiring healthcare associated infections [1]. Ventilator-associated pneumonia (VAP) is lower respiratory tract infection in patients on ventilator support and is responsible for high mortality and morbidity [2]. The commonest microorganisms involved in ventilator-associated pneumonia VAP are Gram negative organisms like *Klebsiella pneumoniae*, *Pseudomonas*, *Acinetobacter species*, *Escherichia coli* while *Staphylococcus aureus* is the most common Gram-positive pathogen. Prolonged admission in ICUs can lead to infections with multiple microorganisms which may complicate the therapy of the patients and lead to antibiotic resistance [3].

Updated knowledge of local epidemiology

and bacterial spectrum from endotracheal secretions is essential for preparing guidelines for empirical treatment of patients in ICUs who develop VAP. Identification of pathogens by culture is the gold standard for the treatment of these critically ill patients [1]. The purpose of the present study was to identify etiological profile of bacteria causing VAP in our hospital.

## MATERIAL AND METHODS

The study was conducted in Microbiology Department of Lahore General Hospital from January to December 2017. 445 specimens of endotracheal secretions were received from patients suspected of VAP. American Thoracic Society (ATS) and Infectious Diseases Society of America (IDSA) guidelines recommend culture of tracheal secretions for lower respiratory tract infections. These samples also describe the clinical criteria for diagnosing VAP, according to 'clinical pulmonary infection score' (CPIS). The clinical, physiological, microbiological and radiographic evidence provide the numerical value for presence or absence of VAP. The scoring system can range between 0 to 12 and the score of  $\geq 6$  shows good correlation with the presence of VAP

**Correspondence:** Dr Muna Malik, Ameer ud din Medical College/ Post Graduate Medical Institute, Lahore General Hospital, Lahore Pakistan

Email: [mmkamboh@hotmail.com](mailto:mmkamboh@hotmail.com)

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[4]. A positive endotracheal secretion culture along with pulmonary infiltration, fever and/or leukocytosis is sufficient to diagnose VAP [5].

Patients admitted in ICUs for more than 48 hours of either gender or age, having fever  $\geq 38^{\circ}\text{C}$ , whose WBCs count was  $\geq 10,000/\text{mm}^3$  or  $\leq 3000/\text{mm}^3$ , having purulent tracheal secretions and with diffused or patchy infiltration in chest radiograph were included in our study.

Patients clinically diagnosed and having radiological signs of pneumonia before hospital admission, patients with other respiratory tract infections, confirmed cases of pulmonary tuberculosis and immunocompromised patients were excluded from the study.

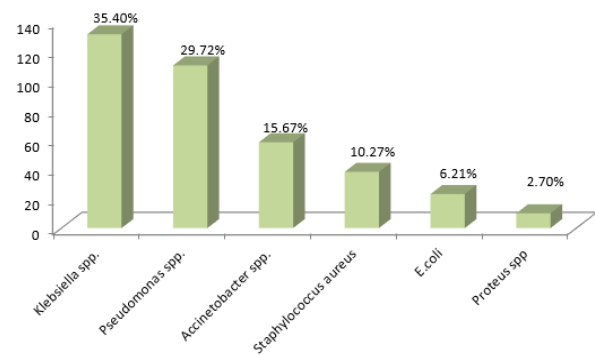
According to Centers for Disease Control (CDC) a culture is considered positive when more than  $10^5$  colony-forming units (CFU)/mL of a bacteria are isolated on culture and/or more than 25 polymorph nuclear cells per low-power field is seen on direct smear of endotracheal secretion [6]. After Gram staining [7], the samples were inoculated on blood and MacConkey agar with added crystal violet, and incubated up to 48 hours at  $37^{\circ}\text{C}$ . The cultures were read as semi quantitatively when growth was moderate or heavy and quantitatively when more than  $10^5$  colony-forming units CFU /mL of bacteria were isolated. The isolates were identified by standard microbiological procedures [1, 8].

## RESULTS

A total of 445 tracheal secretions were processed, collected from 365 (82%) male and 80 (18%) female patients. The mean age was  $50 \pm 15$  years. 370 samples (83%) yielded growth on culture. Of these, 75 (20.3%) were polymicrobial.

Figure 1 shows that the most common bacterium isolated from tracheal secretion on culture were *Klebsiella pneumoniae* 131 (35.4%), followed by *Pseudomonas aeruginosa* 110 (29.7%) *Acinetobacter spp.* 58 (15.7%), *Staphylococcus aureus* 38 (10.3%), *E. coli* 23 (6.2%) and *Proteus spp.* 10 (2.7%).

The most common mixed growth of two types of bacteria was *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* (43%). 14 (21.5%) samples had mixed growth of *Pseudomonas aeruginosa* and *Acinetobacter spp.* Other patterns of mixed growth were *Klebsiella spp.* and *Acinetobacter spp.*, *Acinetobacter spp.* and *E.Coli*, *Klebsiella spp.* and *E.coli*, *Staphylococcus aureus* and *Klebsiella spp.*, *E.coli* and *Pseudomonas spp.*



**Figure-1: Bacterial isolates from endotracheal secretions (n=370).**

## DISCUSSION

Despite advancement in preventive approaches, diagnostic systems and treatment plans, ventilator-associated pneumonia (VAP) remains the most prevalent infectious problem among patients admitted in intensive care units [9]. Nosocomial infection rate is progressively rising in ICU admitted patients due to excessive use of invasive procedures performed on them including artificial ventilator support [10].

In our study, male predominance is seen among the samples of tracheal secretion received from ICU admitted patients. This could be because most of the working community is composed of males and that is non-modifiable factor associated with VAP [9]. Majority of the samples in our study were received from Punjab Institute of Neurosciences (PINS). The reason for this could be that Lahore General Hospital is the major center of neurosciences. These patients often require ventilator support, which can lead to VAP. A similar preponderance of critically ill patients suffering from brain trauma has been reported by Mehndiratta et al [11]. Proper collection and culture of tracheal secretions can give a timely diagnosis and improve the clinical outcome for these patients. Mohanty et al have reported that trans-tracheal aspirates yielded a large number of positive culture growth in their patients [12].

In our study, 75 samples yielded polymicrobial growth. The reason for mixed growth could be that ICU patients had a prolonged stay at hospital and they underwent multiple invasive procedures like artificial ventilation along with central venous lines or catheterization. These invasive procedures allow introduction of multiple microbial pathogens, which can flourish in these immunocompromised patients. This observation was also reported by Saddique et al in 2017 [1].

The commonest bacterium, which was isolated from tracheal secretions in the present study was *Klebsiella pneumoniae*. Many studies also documented *Klebsiella spp.* as the most frequent bacteria isolated from tracheal secretions [13,14]. The spectrum of bacterial isolates in our study is similar to what has been reported by other authors [9, 15]. In our study, mixed bacterial growth of two types of bacteria and three types of bacteria was also observed. Poor hygiene practice, prolonged hospital stay, immunocompromised status of patients and absence of cough reflex might be responsible for biofilm formation in endotracheal tubes, allowing these bacteria to travel down the lower respiratory tract and lead to ventilator-associated pneumonia [16]. Koirala et al have also reported a polymicrobial spectrum of isolates from endotracheal secretions similar to our results [17].

## CONCLUSION

Gram negative bacilli are the commonest pathogens isolated from the endotracheal secretions of patients with ventilator-associated pneumonia. VAP is a preventable condition so the need of the hour is to strengthen our infection control practices in our hospital settings to reduce prevalence of these bacteria among critically ill patients. Regular studies should be conducted in hospital so that etiological pattern and antibiogram are clinically audited and following the guidelines of infection control, we can decrease mortality and morbidity in hospital patients.

## AUTHORS CONTRIBUTION

**Muna Malik:** Sample collection, data analysis, literature review and write-up.

**Muhammad Irfan Malik:** Planned research work, literature review.

**Ayesha Sajjad:** Literature review.

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