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Multiresistance Determinants of Bacterial Agents in Patients with Nosocomial Pneumonia

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Abstract

Nosocomial pneumonia is recognized as a common and serious complication in hospitals and other healthcare settings across the globe**.** It is one of the most common hospital-acquired infections, particularly among patients in intensive care units. The emergence of antibiotic-resistant bacteria, such as methicillin-resistant *Staphylococcus aureus* (MRSA) and multidrug-resistant Gram-negative bacteria (*Pseudomonas aeruginosa, Acinetobacter baumannii* and extended-spectrum beta-lactamase (ESBL)-producing *Enterobacteriaceae)*, poses a growing challenge in the management of this infection. These pathogens may colonize healthcare environments and present a risk to hospitalized patients, especially those with underlying health conditions or undergoing invasive procedures.

Our research aimed to identify the predominant causative agents, to determine extended-spectrum beta-lactamases, and inducible clindamycin resistance in patients with nosocomial pneumonia while also contrasting these findings with isolates obtained from cases of community-acquired pneumonia (CAP). The study findings reveal a diverse bacterial spectrum associated with nosocomial pneumonia. Gram-negative bacteria were more prevalent (90.0% of cases), with P.aeruginosa being the most dominant (in 36.6% of cases). In cases of CAP, more prevalent was Gram-positive bacteria (80.0%). Among Gram-negative strains, ESBL, a key factor in multidrug resistance, was frequently identified at 88.8%, notably in all *P. aeruginosa* and *A. baumannii* strains. Additionally, MRSA strains with ICR, another determinant of multiresistance, were isolated from all staphylococcal strains obtained from patients with nosocomial infections. Identifying causative pathogens and their antimicrobial resistance determinants leads to antibiotic therapy and is crucial for improving patient outcomes and reducing the burden of healthcare-associated infections.

Key words: Nosocomial pneumonia, community-acquired pneumonia, Gram-negative bacteria, Gram-positive bacteria, *Mycoplasma pneumoniae,* extended-spectrum beta-lactamase, inducible clindamycin resistance

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Introduction

Nosocomial pneumonia is a significant concern worldwide, contributing to healthcare-associated infections and associated morbidity, mortality, and healthcare costs. It is a leading cause of healthcare-associated infections worldwide. The prevalence, incidence, and management of nosocomial pneumonia can vary across different countries due to factors such as healthcare infrastructure, infection control practices, antibiotic usage patterns, patient demographics, and socioeconomic conditions. Mortality rates can vary depending on factors such as the causative pathogen, patient comorbidities, and the adequacy of treatment [3, 6, 11].

Risk factors for developing nosocomial pneumonia include prolonged hospitalization, mechanical ventilation (ventilator-associated pneumonia), older age, underlying health conditions (such as chronic lung disease or immunosuppression), invasive procedures, aspiration of secretions, compromised immune defenses [5, 9, 10]. Common pathogens associated with nosocomial pneumonia include bacteria such as *Staphylococcus aureus* [11], *Pseudomonas aeruginosa* [12,18], *Acinetobacter baumannii* and *extended-spectrum beta-lactamase* (ESBL)-producing *Enterobacteriaceae* [2, 7, 12], as well as viruses and fungi in some cases Treatment for nosocomial pneumonia typically involves antibiotics targeted at the specific pathogens identified through cultures and sensitivity testing. They play an important role in the formation of bacterial multidrug resistance [1,4]. Among nosocomial bacterial strains, ESBL expression significantly increased in many countries. These bacteria are often resistant to different groups of antibiotics, which makes it difficult to develop an effective treatment regimen [1,8].

Furthermore, nosocomial infections are often associated with multidrug-resistant bacteria, which may harbor additional resistance mechanisms alongside inducible clindamycin resistance (ICR), especially in *Staphylococcus aureus* and *Streptococcus pneumoniae* strains. The presence of ICR can further limit the available treatment options, making it challenging to manage infections caused by these bacteria [18].

However, antibiotic resistance poses a significant challenge in the management of nosocomial pneumonia, requiring careful selection of antibiotics and adherence to antimicrobial stewardship practices. Nosocomial pneumonia is a significant concern in healthcare systems worldwide, and its incidence and management can vary between countries due to factors such as healthcare infrastructure, infection control practices, antibiotic usage patterns, and prevalence of antibiotic-resistant bacteria. While the incidence and management of nosocomial pneumonia may vary between countries, it remains a global healthcare issue requiring concerted efforts to improve infection prevention, antimicrobial stewardship, and patient outcomes.

Community-acquired pneumonia (CAP) causes morbidity and mortality globally and can affect individuals of all ages, although certain groups, such as the elderly, young children, and those with underlying chronic diseases (such as COPD, diabetes, or heart disease), smoking, immunosuppression,

and recent viral respiratory infections are at higher risk. The incidence and prevalence of CAP can vary depending on factors such as geographic location, climate, and circulating pathogens. CAP has a good prognosis with appropriate treatment, although severe cases can lead to complications, hospitalization, or death, particularly in high-risk populations. The most common pathogens responsible for CAP include *Streptococcus pneumoniae* (the leading cause of CAP) [15,17], *Haemophilus influenzae, Mycoplasma pneumoniae, Chlamydia pneumoniae,* and respiratory viruses such as influenza, Coronaviruses, and respiratory syncytial virus [16,17]. The specific causative agent may vary depending on factors such as age, underlying health conditions, and recent antibiotic use. The identification of the causative pathogen can help guide appropriate treatment decisions. Identifying causative agents of nosocomial pneumonia, determining local antibiotic resistance strains, management, and prevention strategies can vary widely depending on regional factors.

Our study aims were to identify the most common causative pathogens, the presence of extended-spectrum beta-lactamases, inducible clindamycin resistance in patients with nosocomial pneumonia and compare these results with isolates obtained from patients with CAP.

Material and Methods: The study was conducted on the blood and sputum of 60 patients with nosocomial pneumonia and CAP. Microbiological examination and results analysis were conducted in the Medical Company "Test-IMP" and the Microbiology Department of TSMU. There were identified 60 different strains of Gram-positive, Gram-negative bacteria, and *M. pneumoniae*. They were identified by standardized identification systems (BioMérieux, France - API 20E, API 20NE. API HARN, API 20XXE) and serological methods (immunochromatographic test) under the recommendations of the European Committee on Antimicrobial Susceptibility Testing (EUCAST) [13,14].

Results and discussion: There were identified four bacterial species isolated from 30 patients with nosocomial pneumonia. The results are summarized in diagram N1, which illustrates that *P. aeruginosa* (11 strains, 36.7% was the most frequently isolated. *K. pneumoniae* and *A. baumannii* were isolated in relatively small and equal numbers (each - 8 strains, 26.6%). *S. aureus* was isolated in the lowest numbers (3 strains, 10.0%. Gram-negative bacteria were much more frequent (27 strains, 90,0%) than Gram-positive (3 strains, 10.0%).

Diagram N1. Bacterial species isolated from patients with nosocomial pneumonia

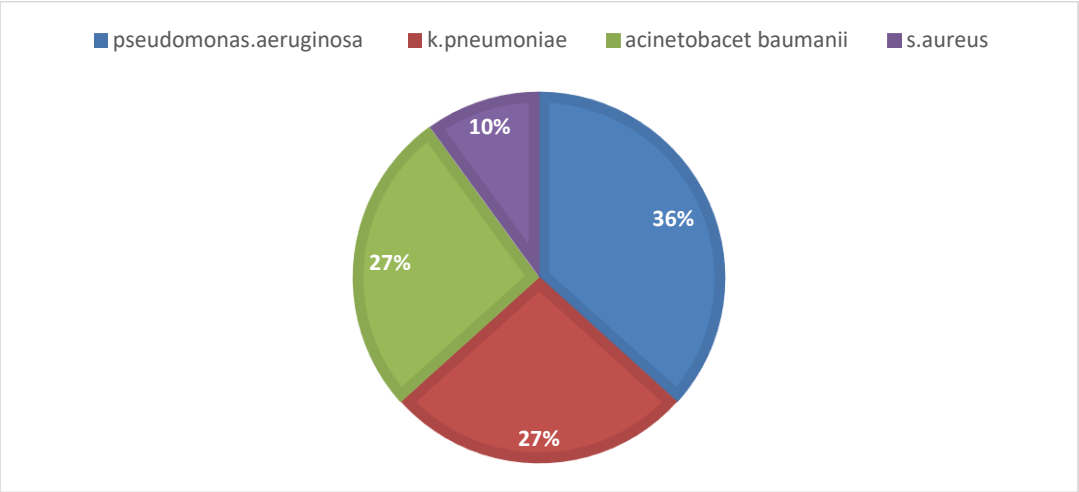
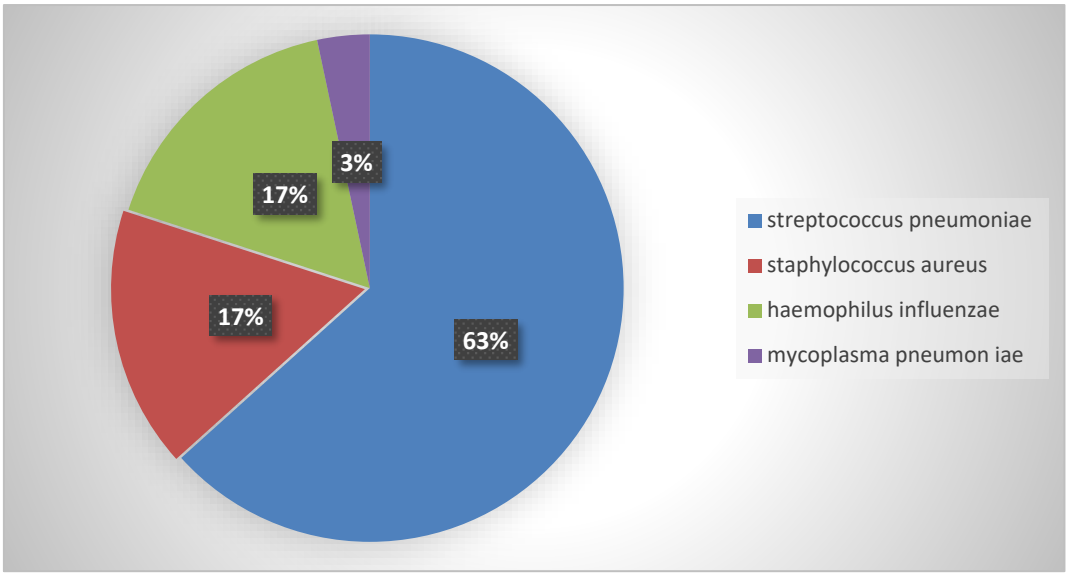


Diagram N2 demonstrates bacterial species isolated from 30 patients with CAP. The findings indicate that *S. pneumoniae* (19 strains, 63.3%) was the most commonly isolated organism in CAP patients. *H.*

influenzae and *S. aureus* were found in comparatively lower and equal frequencies (each - 5 strains, 16.6%). M. pneumoniae was identified in one case (3%). Gram-positive bacteria were much more frequent (24 strains, 80,0%) than Gram-negative (5 strains, 16.6%).

Diagram N2. Bacterial species isolated from patients with CAP



Also, has been investigated the prevalence of Gram-negative bacterial ESBLs isolated in patients with nosocomial pneumonia. A total of 24 ESBL-positive bacterial strains were isolated from 27 Gram-negative strains, representing 88.8%. By species, the frequency of their detection was distributed as follows: *P. aeruginosa* - 100%, *A. baumannii* - 100%, and *K. pneumoniae* – 62.5%. Results are shown in table N1.

Table N1 Frequency of Gram-negative bacterial ESBLs in patients with nosocomial pneumonia.

Bacterial species	abs. n.	%
P. aeruginosa n=11	11	100
A. baumannii n=8	8	100
K. pneumoniae n=8	5	62.5

ICR was identified in both nosocomial- and CAP-isolated *S. aureus* strains. All isolated staphylococci were MRSA strains with ICR (5 cases, 100%) in patients with nosocomial infection and only 1 MRSA with ICR (20.0%) was revealed in CAP-diagnosed patients.

Conclusion: According to the results of the study, the bacterial spectrum of infection in patients with nosocomial pneumonia is quite diverse and consists of four types of Gram-positive and Gram-negative microorganisms. Infection was caused more often by Gram-negative bacteria (90.0%) and *P. aeruginosa* was dominant (36.6%). In isolates from CAP infection, more prevalent was Gram-positive bacteria (80.0%). In Gram-negative strains, one of the factors determining multidrug resistance, ESBL, was detected quite often (88.8%). They were detected in all *P. aeruginosa* and *A. baumannii* strains. Also, another multiresistance determinant, MRSA strains with ICR, were isolated in all staphylococcal strains isolated from patients with nosocomial infection.

Determining the microbial etiology of nosocomial pneumonia, including the prevalence of specific

bacteria, helps guide infection control measures and antibiotic therapy strategies.

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