

ANTIBIOTIC RESISTANCE – A 21ST CENTURY THREAT

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Keywords: *microorganisms, antibiotics, antibiotic susceptibility, microbiology, bacteria.*

RELEVANCE

The discovery of penicillin by Alexander Fleming in 1928 and its subsequent isolation by Howard Florey and Ernst Chain in 1945 marked the beginning of a new era in the treatment of infectious diseases—antibacterial therapy. However, to date, more than 20–40% of antibacterial drugs are prescribed without adherence to the principles of rational antibiotic therapy. These principles include strict indications for drug administration, appropriate dosing and duration of treatment, and consideration of drug compatibility, among others. Globally, more than 700,000 deaths per year are attributed to infectious diseases, primarily caused by antibiotic-resistant bacterial strains. Respiratory tract infections have become among the most frequently encountered diseases, including within the structure of hospital-acquired infections.

OBJECTIVE:

The aim of this study was to assess the prevalence and antibiotic resistance of the most common microbial strains isolated from respiratory tract samples (nasopharyngeal swabs and sputum) of patients with respiratory infections.

MATERIALS AND METHODS

A total of 225 microbial strains were analyzed, obtained from 69 patients (both male and female) aged 18 to 65 years, diagnosed with respiratory diseases such as bronchitis, pharyngitis, and tracheitis. The study focused on respiratory tract secretions, including phlegm and nasopharyngeal swabs.

Laboratory Analysis:

The laboratory investigations were conducted at the Department of Microbiology and Pharmacology in the “Microbiology and Immunology” laboratory of the Research Center for Maxillofacial Surgery. The analysis included microbial isolation, identification, and assessment of antibiotic susceptibility.

RESULTS AND DISCUSSION

A significant species diversity of detected pathogens was established, with a total of 13 identified species. Throughout the study period, infections caused by a single pathogen were observed in 33.2% of cases, while the remaining cases were mixed infections (bacterial and viral co-infections). The most frequently isolated pathogens were *Klebsiella pneumoniae* (10.3%), *Staphylococcus aureus* (6.3%), and *Proteus mirabilis* (1.4%). The prevalence of

Pseudomonas aeruginosa (5.5%), *Staphylococcus haemolyticus* (1.6%), and *Enterococcus faecalis* (1.5%) was also noted.

Staphylococcus aureus is a group of Gram-positive, immobile microorganisms that do not form spores or capsules. Methicillin-resistant *Staphylococcus aureus* (MRSA) strains, which are resistant to all β -lactam antibiotics, also exhibit associated resistance to fluoroquinolones, macrolides, aminoglycosides, lincosamides, and tetracyclines. The analysis of isolated *S. aureus* strains revealed an increase in resistance to amikacin by 29.1%, cefuroxime by 35.0%, levofloxacin by 17.5%, oxacillin by 27.8%, and erythromycin by 6.4%. A decrease in resistance was observed for amoxicillin/clavulanic acid (by 6.9%) and trimethoprim-sulfamethoxazole (by 12.2%).

The analysis of *Klebsiella pneumoniae* susceptibility to antibiotics demonstrated resistance to amikacin in 12% of cases, meropenem in 27.3%, imipenem in 24.6%, ceftazidime in 35.3%, amoxicillin/clavulanic acid in 21%, tigecycline in 100%, and levofloxacin in 19.2%. Simultaneously, a reduction in resistance was observed for ampicillin (by 11.5%), trimethoprim-sulfamethoxazole (by 0.2%), and ciprofloxacin (by 18.5%).

In patients with isolated *Proteus mirabilis*, resistance was recorded for amikacin (16.8%), meropenem (2.7%), imipenem (1.5%), amoxicillin/clavulanic acid (20.6%), levofloxacin (4.6%), ciprofloxacin (39.6%), ampicillin (15.2%), ceftazidime (12.8%), and trimethoprim-sulfamethoxazole (10.0%).

The Gram-negative bacterium *Pseudomonas aeruginosa* is an obligate aerobe known for its high resistance to multiple antimicrobial agents. Analysis of the obtained data indicated an increase in resistance of these strains to amikacin by 52.5% (from 43.1% to 95.6%), imipenem by 82.6% (from 9.7% to 92.3%), amoxicillin/clavulanic acid to 100%, meropenem by 71.5% (from 23.6% to 95.1%), ertapenem to 100%, and cefotaxime by 76.4% (from 13.6% to 90.2%).

CONCLUSION

Given the global spread of resistance determinants to clinically significant antibiotics, it is essential to integrate *Klebsiella pneumoniae* and *Staphylococcus aureus* into antibiotic resistance surveillance systems at all levels as key indicators of overall population resistance.

In accordance with modern strategies for rational antibiotic therapy, continuous monitoring of antimicrobial resistance, identification of resistant strains, and the widespread implementation of accelerated laboratory diagnostics for bacterial resistance markers remain crucial. Furthermore, to enhance the effectiveness of treatment in patients with chronic respiratory infections, the integration of alternative therapeutic approaches—such as physiotherapy, phytotherapy, and bacteriophage therapy—should be actively promoted in clinical practice.

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