ANTIMICROBIAL RESISTANCE IN CLINICAL STRAINS OF *PSEUDOMONAS AERUGINOSA*

Cristian ROSIORU, Ion BERDEU, Greta BALAN

Nicolae Testemitanu State University of Medicine and Pharmacy, Chisinau, Republic of Moldova

Corresponding author: Cristian Roșioru, e-mail: rosiorucristian1478@gmail.com

Keywords: *Pseudomonas aeruginosa, resistance, antimicrobial agents.*

Introduction. *Pseudomonas aeruginosa* stands out as a predominant pathogen causing nosocomial infections, particularly in patients with underlying pathologies or compromised immune systems. The eradication of *P. aeruginosa* has become increasingly challenging, given its remarkable resistance to antibiotics. Strains of *P. aeruginosa* deploy both intrinsic and acquired resistance mechanisms, making them formidable against a wide array of antibiotics. Furthermore, adaptive antibiotic resistance in *P. aeruginosa*, a recently characterized mechanism, involves biofilm-mediated resistance and the formation of multidrug-tolerant persisted cells, contributing to infection relapse. Carbapenem-resistant *P. aeruginosa* has been identified by the World Health Organization as one of three bacterial species urgently requiring the development of new antibiotics. The overuse of antibiotics in treatment exacerbates the development of multi-drug-resistant *P. aeruginosa* strains, rendering empirical antibiotic therapy ineffective against this microorganism.

Aim. Determination of resistance profiles in *Pseudomonas aeruginosa* strains isolated from clinical bio substrates.

Material and methods. The antimicrobial susceptibility profiles of *P. aeruginosa* isolates were determined using the standard disk diffusion method, following the guidelines outlined by the European Committee on Antimicrobial Susceptibility Testing (EUCAST 2022). An isolate was classified as multidrug-resistant (MDR) if it demonstrated resistance to at least one antimicrobial agent in three or more distinct antibiotic classes. For quality control, the reference strain *P. aeruginosa* (ATCC 27853) was employed.

Results. They analyzed 765 isolates from patients hospitalized in surgical wards. These strains were isolated from various pathological products, including the lower respiratory tract, pus, peritoneal fluid, urine, central venous catheter insertion, blood, feces, bile, and other secretions. *P. aeruginosa* strains exhibited the following levels of antibiotic resistance: 90.3% to ticarcillin, 78.5% to piperacillin, and 89.6%, respectively 66.8%, to penicillin's combined with beta-lactamase inhibitors (ticarcillin with clavulanic acid and piperacillin with tazobactam). Resistance to antipseudomonal cephalosporins was observed at 67.6% for ceftazidime and 69.2% for cefepime, while resistance to carbapenems was 68.0% for imipenem and 58.2% for meropenem. Aminoglycoside resistance rates were 52.0% for gentamicin, 67.6% for tobramycin, and 46.4% for amikacin. Notably, 78.5% of strains exhibited cross-resistance to fluoroquinolones (ciprofloxacin, levofloxacin, moxifloxacin, norfloxacin), while resistance to colistin was only 8.4%. A significant majority, 697 strains of *P. aeruginosa* (91.0%), were classified as multidrug-resistant (MDR).

Conclusions. The restricted susceptibility to antimicrobial agents and the frequent emergence of antibiotic resistance during therapy have significantly complicated the treatment of *Pseudomonas aeruginosa* infections. Consequently, continuous monitoring of drug resistance development in this organism group is of paramount importance. Additionally, the prudent and careful use of antimicrobial agents is imperative to counteract the progression of antimicrobial resistance.

Note: This paper has been written within the framework of the project: 20.80009.8007.09 "Studying the mechanisms of antimicrobial resistance in gram-negative bacilli in order to strengthen the national surveillance system"