GLOBAL AND UKRAINIAN DATA ON MULTIDRUG RESISTANCE IN *PSEUDOMONAS AERUGINOSA*

Kravchenko A.[1], **Zelena L.**[1,2], **Tkachuk N.**[3]
[1] Open International University of Human Development "Ukraine", Kyiv, Ukraine
[2] D.K. Zabolotny Institute of Microbiology and Virology of the NAS of Ukraine, Kyiv, Ukraine
[3] T.H. Shevchenko National University "Chernihiv Colehium", Chernihiv, Ukraine
Anddrrey@ukr.net

Antibiotic resistance in bacteria represents one of the most serious threats to modern medicine, complicating the treatment of infectious diseases and creating significant challenges for healthcare systems worldwide. According to the World Health Organization (WHO), antibiotic resistance causes approximately 700,000 deaths annually, and without effective treatment this value can reach 10 million deaths per year by 2050. The problem is particularly acute in cases of nosocomial infections caused by Gram-negative bacteria, among which *Pseudomonas aeruginosa* is distinguished by its exceptional ability to adapt and develop multidrug resistance (MDR). *P. aeruginosa* is a Gram-negative opportunistic pathogen characterized by high ecological plasticity, the ability to survive under diverse conditions, and significant pathogenic potential. It is one of the causative agents of hospital infections such as ventilator-associated pneumonia, urinary tract infections, wound infections, and sepsis. The multidrug resistance of *P. aeruginosa* makes it resistant to most classes of antibiotics, which greatly complicates therapy and increases the risk of adverse clinical outcomes.

The molecular basis of antibiotic resistance in this bacterium includes a wide range of genetic adaptations. The main mechanisms are mutations in genes encoding efflux pumps, enzymes that inactivate antibiotics, modifications of antibiotic targets, and changes in cell membrane permeability. In Ukraine, the problem of *P. aeruginosa* antibiotic resistance remains insufficiently studied, although the growing number of hospital infections, limited availability of modern antibiotics, and high levels of antibacterial drug use highlight the relevance of studying local isolates.

The aim of this study was to conduct a systematic analysis of the prevalence of multidrug-resistant *P. aeruginosa* strains worldwide and to investigate the spectrum of mutations in genes responsible for multidrug resistance in Ukrainian isolates. A systematic literature review was performed using the PubMed database with keywords related to *P. aeruginosa* antibiotic resistance. For bioinformatic analysis, the NCBI, PATRIC, and CARD databases were used, along with BLAST, Clustal Omega, ResFinder, and AMRFinderPlus tools. Statistical processing was carried out using t-test, ANOVA, and correlation analysis.

The results of the analysis revealed that the proportion of resistant *P. aeruginosa* isolates worldwide is 50% in Europe and over 60% in Asia, while in Ukraine the level of MDR isolates in hospital settings is 20–25%. Statistical analysis confirmed the dominance of combined resistance mechanisms and the spread of high-risk international clones ST235 and ST111. It was established that the most common multidrug resistance genes among Ukrainian isolates are: *oprD* (mutation frequency 72.4%), *gyrA/parC* (58.7%), *mexR/nalC* (46.2%), and β-lactamase genes (38.9%). Types of mutations include point substitutions (predominantly in *gyrA* – Ser83Leu, *parC* – Ser87Leu), deletions/insertions (*oprD*), and overexpression of regulators (*mexR*, *nalC*). The obtained results can be used to improve strategies for diagnosis, prevention, and treatment of infections caused by multidrug-resistant *P. aeruginosa* strains.