Antimicrobial Resistance of Lactose Non-Fermenting Gram-Negative Bacteria Causing Hospital-Acquired Infections in Neurosurgical Patients

Thesis

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ABSTRACT

The extensive and indiscriminate use of antibiotics has led to the emergence of non-fermentative gram-negative bacilli (NFGNB) as significant hospital-acquired infection pathogens. They have been linked to infections such as meningitis, pneumonia, septicemia, urinary tract infections, and surgical site infections. Multidrug-resistant (MDR) pathogens are typically the outcome of broad-spectrum antibiotics. As a result, we are addressing rising MDR NFGNB rates linked to extended hospital stays, greater expenses, and higher mortality. *P.aeruginosa* and *A.baumannii* are the two most significant MDR pathogens.

The World Health Organization's list of critical priority infections includes *P.aeruginosa* and *A.baumannii*. Carbapenem-resistant *P.aeruginosa* and carbapenem-resistant *A.baumannii*, the majority of which are also MDR or XDR pathogens, are particularly troublesome pathogens.

The aminoglycosides are the preferred antibacterial medication for severe infections brought on by NFGNB. However, *P.aeruginosa* and *Acinetobacter* species may acquire resistance to aminoglycosides by enzymatic alteration, impermeability, or efflux pumps.

Aminoglycoside resistance genes are genetically and structurally different and are observed among various *P.aeruginosa* and *Acinetobacter* species isolates. The prevalence of 16S RNA methyltransferases, which confer resistance to all aminoglycosides, differs geographically. The predominance of 16S RNA methyltransferases genes as the main aminoglycoside resistance genes in the Egyptian isolates is an essential finding, as it is known that these enzymes confer resistance to all aminoglycosides, including the novel ones. The aminoglycoside resistance genes could easily spread among

NFGNB strains so coordinated effort and current research are needed to manage aminoglycoside resistance before it becomes a serious problem.