ANALYSIS OF ANTIMICROBIAL RESISTANCE IN CLINICAL STRAINS OF *KLEBSIELLA PNEUMONIAE*

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Introduction. In recent years, the resistance of *Klebsiella pneumoniae* species, both to reserve antimicrobials and to several groups of antimicrobial preparations (MDR), has emerged as a significant global public health concern. *K. pneumoniae* exhibits a variety of antimicrobial resistance mechanisms and is a common pathogen responsible for surgical wound infections, gastrointestinal tract infections, urinary tract infections, and community-acquired infections that can trigger nosocomial infection outbreaks. Numerous studies have shown that a majority of infections linked to various medical devices, including urinary and intravascular catheters, were attributed to *K. pneumoniae*, with approximately 90% of these strains being biofilm producers. According to a report by the CDC, of the 9,000 infections caused by carbapenem-resistant Enterobacteriaceae species documented in 2013, around 80% were attributed to *K. pneumoniae*. Currently, the global antimicrobial resistance rate for *K. pneumoniae* is estimated to be approximately 70%, with a mortality rate ranging between 40% and 70%. **Aim.** Determination of resistance profiles and detection of resistance mechanisms in *K. pneumoniae* strains isolated from clinical biosubstrates. **Material and methods.** For the determination of *K. pneumoniae* strains producing extended-spectrum beta-lactamases and/or carbapenemases, phenotypic tests (double disk synergy test, combined disk test (MastDisk Combi), Amp-C test with cloxacillin, Normand Poirel test, MAST CARBA PacE) and molecular genetic tests were performed. Through the Combo Test, Combi Carba Plus tests and the immuno-chromatographic method, the KPC, OXA-48, MBL (NDM, VIM, IMP) type enzymes that confer resistance to the bacteria were highlighted. Confirmation of resistance mechanisms was performed by the molecular-genetic method. **Results.** Between 2020 and 2022, a total of 867 (76.8%) *K. pneumoniae* strains were isolated and reported from urine and 262 (23.2%) strains - from blood and CSF. The resistance profiles of *K. pneumoniae* indicate worrying levels of resistance to all groups of antimicrobial preparations, such as: penicillins – 76.5%, fluoroquinolones – 78.4%, 3rd generation cephalosporins – 82.8%, 4th generation cephalosporins – 64, 1%, aminoglycosides – 71.6%, including carbapenems – 40.5% and colistin – 23.5%. ESBL-producing strains are increasing, from 17.5% confirmed strains in 2020 to 33.6% confirmed isolates in 2022. Among the 66.5% strains suspected of producing carbapenemases, 35.7% isolates were identified by the immunochromatographic method, including OXA-48 type presented 34.4% strains of *K. pneumoniae*, NDM type – 13.9%, IMP type – 4.9% strains, KPC and VIM type – 0.2% strains each. Through the multiplex PCR, 29.4% strains of *K. pneumoniae* with resistance genes were confirmed. In 28.8% of isolates, the blaOXA-48 gene was determined. Alarmingly, 10.0% strains showed 2 or more resistance mechanisms simultaneously. **Conclusions.** *K. pneumonia* is the most common pathogen involved in the etiology of invasive infections. The resistance levels of this species have reached alarming levels, even with reserve antimicrobials. In the investigated *K. pneumoniae* species, a wide array of resistance enzymes was identified, with the most frequent being OXA-48, followed by NDM.