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DISTRIBUTION OF ANTIBIOTIC RESISTANCE GENES IN MICROORGANISMS IN POTABLE WATER-HUMAN ORGANISM CHAIN

The spread of resistant strains in environmental objects (surface and soil waters, bottom deposits, wastewaters, soils) where a large-scale exchange with resistance determinants takes place between clinical strains and natural bacteria, attracts increasingly greater attention of researchers (Amarasiri et al., 2020). The spread of poly- and multiresistant bacteria, pharmaceuticals in environmental objects may serve as a potential source of entry of genetic resistance determinants to human organisms via food chains (Tyagi and Kumar, 2020; Burcea et al., 2020).

Determination of circulation interrelations between antibiotic-resistant microorganisms of *Enterobacteriaceae* family and their resistance genes in clinical strains and potable water samples taken in Uzhhorod and Uzhhorod district.

We carried out generic identification of the microorganisms isolated from clinical samples of the oral cavity of 64 patients suffering from periodontal inflammatory diseases, and potable water samples taken from sources of public centralized and decentralized water supply; the isolated microorganisms were tested for antibiotic sensitivity by the Kirby-Bauer disc diffusion method according to EUCAST. With the help of molecular-genetic methods, the total DNA of potable water was isolated and tested for the presence of the following genetic resistance determinants: carbapenems blaNDM; blaOXA48-like; tetracyclines blaTet-M; cephalosporins blaCTX-M.

In the microbiota of the clinical material and potable water samples, the same spectrum of microorganisms belonging to *Enterobacteriaceae* family dominated; the isolated bacteria showed a high resistance level to beta-lactam antibiotics and to natural antibiotic preparations. The highest level of resistance was established for microorganisms isolated from well water samples, where genetic resistance determinants to blaCTX-M cephalosporins and blaTet tetracyclins were also revealed. The obtained results proved high probability of the spread of antibiotic-resistant microorganisms and their genetic resistance determinants via potable water.

References

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