PATHOGENIC AGENTS OF ACUTE DIARRHEA DISEASE FROM THE ENTEROBACTERIACAEA FAMILY AND THEIR ANTIBIOTIC RESISTANCE

Gutu N.

MTA Buiucani Public Health Medical Institution, Chisinau, Moldova Doctoral school of biological, geonomic, chemical and technological sciences e-mail: nadejda_gutu@mail.ru

CZU:579.61:[579.21+578.2+614.2]

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The Enterobacteriaceae family includes a large number of bacteria that inhabit the intestines of humans and animals, being spread with fecal matter everywhere in the environment. The representatives of the family are characterized by resistance to antibiotics, especially beta-lactam ones (penicillins, cephalosporins, cephamycins and carbapenems), a fact determined by the production of beta-lactamases by these microorganisms.

The aim of this study was to identify the pathogens from the Enterobacteriaceae family, which caused acute diarrheal diseases (ADD) in patients who addressed the AMT Buiucani Public Health Medical Institution during the years 2020-2021, and to highlight the spectrum of antibiotic resistance of isolated specimens.

934 clinical samples (feces) were collected from patients and investigated in the microbiological laboratory of the mentioned institution. Thus, from the positive samples (424) there were isolated and identified pathogenic bacteria (Shigella spp., Salmonella spp.) and conditionally pathogenic bacteria (Klebsiella spp., Proteus spp., Citrobacter spp., Enterobacter spp., Seratia, Providence, Morganella morganii, Pseudomonas aeruginosa) from the Enterobacteriaceae family, which can cause food poisoning and acute diarrheal disease. The sensitivity to antibiotics of the isolated microorganisms was determined by the diffusimetric method with the use of antibiotic sets specific to each pathogen, selected according to EUCAST recommendations and national protocols. The spectrum of resistance of the identified agents is shown in the figure.

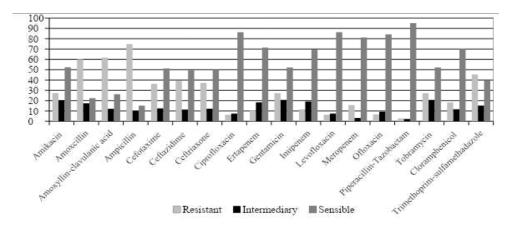


Figure 1. Spectrum of antibiotic resistance of ADD agents

Pathogenic and conditionally pathogenic enterobacteria show a more pronounced sensitivity to such antibiotics as Ciprofloxacin, Levofloxacin and Ofloxacin and increased resistance to Amoxicillin, Ampicillin and Amoxylin – clavulanic acid. As can be seen, cephalosporins become antibiotic-resistant, then aminoglycosides and ampicillins. Resistant bacteria proliferate by natural selection when those sensitive to antimicrobial preparations are removed by antibiotics.

The study was performed within the doctoral project "Pathogens of acute diarrheal diseases - morphocultural features, methods of identification, antibiotic resistance and the dynamics of spread in Chisinau city."