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QUANTITATIVE DETERMINATION OF MICROORGANISMS IN THE INTESTINES OF RATS

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The intestinal microbiome significantly affects the functioning of the body: it participates in metabolic processes, inhibition of pro-inflammatory reactions, in the formation of innate and adaptive immune response in the intestinal mucosa [1-4]. The most important function of the intestinal microbiome is to protect the body from pathogenic microorganisms - pathogens of bacterial intestinal infections [5, 6]. It is known that dysbiotic changes in the intestine lead to increased susceptibility to pathogenic bacteria, such as salmonella [7, 8], which are the etiological factor of gastroenteritis [9]. One of the most common causes of microbiota changes is the use of antibiotics [10-12]. Therefore, of particular interest are the processes of interaction of antibiotics, Salmonella enteritidis and Salmonella typhimurium with representatives of the normal intestinal microflora [13-15]. **The aim** to analyze changes in the quantitative and species composition of the small intestine microbiota in rats with salmonella-induced bowel inflammation on the background of vancomycin and *B. fragilis* administration. **Methods.** All rats, except group I (control, intact), received vancomycin and/or suspension of microorganisms. In order to rapidly internalize bacteria into the intestinal mucosa, the suspension with salmonella was administered orally using a probe. Vancomycin was administered to animals at a rate of 50 mg per kg of body weight, suspensions of microorganisms - in an amount of 15 ml with a concentration of 3x10 8 CFU/g. As a material for bacteriological studies of the intestinal microflora used washes from the ileum of rats. The quantitative and qualitative composition of the wall microbiota in rats by bacteriological method, the statistical analysis of data using the program StatSoft Statistica v12 were conducted. **Results.** The introduction of vancomycin and *S. enteritidis, S. typhimurium* led to changes in the qualitative and quantitative composition of the intestinal microbiome. The introduction of *S. enteritidis* and *S. typhimurium*, on the background of pre-treatment with vancomycin, caused more pronounced changes: increase of the content of *E. coli* 65 and 105 times, *Enterobacter spp., Klebsiella spp., P. aeruginosa* ($p \leq 0.05$), and also a sharp decrease in *Bacteroides spp.* 9 and 10 times, respectively, *Proteus spp.* 17 times, *Peptostreptococcus anaerobius* 20 and 9 times, *Shigella spp.* at 538 and 860 times and *Lactobacillus* at 17 times. Correction of the microflora of rats of *B. fragilis* leads to a sharp decrease of the number of *Salmonella spp., P. aeruginosa, Enterobacter spp., Klebsiella spp., Shigella spp.* ($p \leq 0.05$), *E. coli* 538 times, *Proteus spp.* 322 times, *Acinetobacter spp.* at 6 and 57 times, *Cryptococcus spp.* 7-fold, and increase in *Bacteroides spp., E. faecalis, E. faecium* 10 and 19-fold, *Peptostreptococcus*

anaerobius 7 and 12-fold, *Lactobacillus spp.* 27 and 40 times, respectively.**Conclusions.** When B. fragilis was administered to experimental animals treated with S. enteritidis or S. typhimurium on the background of pre-treatment with vancomycin, a change in the quantitative composition of the microbiota in the parietal contents of the small intestine was observed, namely: a decrease in Salmonella spp., E. coli, P. aeruginosa , Proteus spp., Enterobacter spp., Klebsiella spp., As well as an increase in Bacteroides spp., E. faecalis, E. faecium, Lactobacillus spp. and Peptostreptococcus anaerobius. This prove that the introduction of B. fragilis can be used in the treatment of inflammatory bowel diseases or diseases with impaired barrier function of the intestine.

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