



## The Intestinal Microflora and Antibiotic Therapy

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Since the inception of the global Human Microbiome Project in 2007, which was aimed at deciphering the genome of bacteria inhabiting the human body, 395 phylogenetic groups of microorganisms have been identified and the total number of species is approaching 1500. Among these microorganisms, representatives of the genera *Bacteroidetes*, *Firmicutes* and *Actinobacteria* predominate. However, the gut microbiome contains 400,000 genes, which is 12 times more than the human genome, consisting of 35,000 genes. Normal gut microflora is involved in many functions: synthesis of vitamins and some amino acids, excretion of toxins, regulation of immune response, water-salt metabolism, metabolism of fats and bile acids, bilirubin, calcium. Current data suggest that disorders of intestinal microflora is one of the causes in the occurrence and development of many diseases, which include: necrotizing enterocolitis, opportunistic infections (sepsis, bacteremia, diarrhea, etc.), gastrointestinal tract infections caused by *E. coli*, *Proteus mirabilis*, *Klebsiella pneumoniae*, *Enterobacter spp*, *Pseudomonas aeruginosa*, *Enterococcus*; vulvovaginitis (*Candida spp.*, *E. coli*), urinary infections, antibiotic-associated diarrhea, non-specific ulcerative colitis, Crohn's disease, colorectal cancer, asthma, atopic dermatitis, obesity, type 1 diabetes, etc.

The widespread use of antibiotics worldwide is generally not justified. Literature suggests that about 60 - 80% of patients receive antibiotic therapy without sufficient justification. At the same time there are adverse effects of antibiotics associated with a violation of the composition of the intestinal microflora: impaired regulation of immune homeostasis, reduced food tolerance, metabolic disorder, impaired vitamin absorption, increased susceptibility to infection, development of opportunistic infections, accumulation of antibiotic resistance genes in symbiont microflora. In addition, antibiotics reduce gastrointestinal colonisation resistance. Coloni-

zation resistance is understood as a set of mechanisms that ensure the ability of the microbiota and the macroorganism, cooperatively interacting to protect the ecosystem from pathogenic microflora. The violation of colonization resistance is one of the triggering factors of various diseases.

Another important problem is the strengthening of the pathogenicity of some bacteria under the influence of antibiotics and the appearance of antibiotic-resistant strains of microorganisms, whose number is steadily growing. Thus, according to some projections, up to 10 million deaths from diseases caused by antibiotic-resistant pathogens are expected in 2050. The prevention and correction of microbiota disorders include three main areas: the use of probiotics, faecal microbiota transplantation and phage therapy. The use of probiotics helps to normalize the composition of the intestinal microflora, increase colonization resistance to pathogenic and opportunistic microorganisms, regulate local and systemic immunity, reduce intestinal mucosal permeability and increase the production of secretory IgA and anti-inflammatory cytokines.

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