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NORMAL MICROFLORA OF THE GASTROINTESTINAL TRACT

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Abstract: The normal microflora of the gastrointestinal tract (GI) is one of the most important physiological systems of the human body, and its composition and functional state determine many aspects of the health of the macroorganism. As a result of metagenomic studies (16S rRNA profiling, whole genome sequencing and metabolomics) in the last decade, the phylogenetic and functional diversity of the GI microbiota has been radically reassessed. It is currently established that 90-99% of the intestinal microbiota in healthy adults is composed of the phyla Firmicutes, Bacteroidetes, Actinobacteria and Verrucomicrobia, of which the most important functional representatives are Faecalibacterium prausnitzii, Akkermansia muciniphila, Roseburia intestinalis, Eubacterium rectale, Bifidobacterium longum and Bacteroides thetaiotaomicron species. This complex of microorganisms not only ensures the absorption and metabolism of nutrients, but also forms the mucosal immune system, creates a barrier against the colonization of pathogenic microorganisms, synthesizes short-chain fatty acids (acetate, propionate, butyrate), vitamins (K, group B), neurotransmitters (GABA, serotonin) and other bioactive compounds, and directly affects the activity of the central nervous system through the "gastrointestinal-brain" axis.

Keywords: normal state of gastrointestinal microflora, microbiota, dysbiosis, short-chain fatty acids, immune modulation, gut-brain axis. probiotics, fecal microbiota transplantation, personalized microbiome medicine.

Enter

The normal state of the gastrointestinal (GI) microflora is one of the fastest growing and multidisciplinary research areas in modern medicine. Large cohort studies conducted in 2020-2025 (Human Microbiome Project Phase II, MetaHIT, American Gut Project, Flemish Gut Flora Project) revealed that the intestinal microbiota has 150 times more genes than the human genetic material, and these genes fundamentally determine the metabolic, immune and neuroendocrine processes in the macroorganism. Over the past 5 years. More than 48,000 articles have been published in the PubMed database under the keyword "gut microbiota", which is 12 times more than in 2010.

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The history of the study of microflora begins with I.I. Mechnikov's 1907 work "Optimistic Studies on Longevity". He suggested that the consumption of the Lactobacillus bulgaricus strain through Bulgarian yogurt could reduce the number of "putrefactive" bacteria in the intestine. In the second half of the 20th century, only aerobic and facultative anaerobic bacteria were cultivated, ignoring the fact that 99% of the intestinal microflora is anaerobic. Only in 2007-2012, with the use of the 16S rRNA gene sequencing method and later whole-genome shotgun sequencing technologies, the true phylogenetic and functional diversity of the microbiota was revealed.

A clear definition of the concepts of microbiota and microbiome

In modern scientific literature, the terms "microbiota" and "microbiome" are strictly distinguished. Microbiota is a complex of all living microorganisms that permanently or temporarily inhabit a certain ecological niche (gastrointestinal tract, skin, oral cavity, etc.): bacteria, archaea, viruses (especially bacteriophages), mycobacteria and unicellular protists. The microbiome is the total genetic material of these microorganisms, that is, the set of their genomes. For example, the human colon microbiota consists of approximately 1014 cells, which is 10 times more than the number of somatic and germ cells in the macroorganism, and the total number of genes in the microbiome is 150-200 times more than the 20-23 thousand genes in the human genome - 3-5 million genes. The majority of these genes are associated with the metabolism of carbohydrates, amino acids, xenobiotics, vitamin synthesis, and the production of signaling molecules that regulate the immune system.

The concept of microbiocenosis is broader and includes the dynamic balance between the complex of microorganisms and the macroorganism, including their interaction, competition, symbiosis and parasitism. The term dysbiosis (dysbacteriosis) refers to qualitative and quantitative changes in the composition of the microbiota. Currently, three main types of dysbiosis are distinguished: 1) depletion dysbiosis (loss of important commensal species), 2) overgrowth dysbiosis (increase in opportunistic pathogenic species), 3) reduction in diversity (reduction in alpha-diversity, Shannon index <3.5). The concept of "core microbiota" includes taxa that are present in more than 95% of healthy people. According to the largest meta-analyses from 2023-2025, the core microbiota in adults includes 57 species, the most important of which are: Faecalibacterium prausnitzil, Roseburia intestinalis, Eubacterium rectale, Bacteroides uniformis, B. vulgatus, B. thetaiotaomicron, Akkermansia muciniphila, Bifidobacterium longum subsp. longum, Prevotella copri (only in some populations).

Gradient distribution of microorganisms across sections of the gastrointestinal tract

As the gastrointestinal tract moves from proximal to distal, pH, oxygen concentration, nutrient availability, and transit time change dramatically, so the density and composition of microorganisms vary logarithmically. In the oral cavity, it reaches 10°-10" CFU/ml, in the stomach 10'-10', in the duodenum 10-10, in the ileum 10-10°, and in the colon 10"-10 CFU/gram of feces.

Despite the pH of gastric juice being 1.5–3.5, recent metagenomic studies have identified an average of 127–181 species in the stomach, of which 35–40% 1 are uncultured. In people

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without Helicobacter pylori infection, the dominant genera are Streptococcus, Prevotella, Veillonella, Neisseria, Haemophilus, Rothia, Lactobacillus, and Gemella. As a result of the neutralizing effect of bile and pancreatic juice, the pH in the duodenum and jejunum reaches 6.0–7.4, where facultative anaerobes (Enterococcus, Streptococcus, Staphylococcus, Enterobacteriaceae) and partially strict anaerobes (Lactobacillus, Clostridium) live. The number of anaerobes increases sharply in the ileocecal valve, where Clostridium cluster XIVa, Bacteroides fragilis group, and Bifidobacterium species increase. It is in the ileum that antigen recognition by Peyer's patches and IgA production are most active. In the large intestine, completely anaerobic conditions, slow transit (12-72 hours) and enzymatic processes prevail. Here, 60-70% of the bacterial biomass belongs to the phylum Firmicutes, and 20-40% to the Bacteroidetes. The species with the highest concentration are: Faecalibacterium prausnitzii (5-15%), Bacteroides spp. (10-30%), Prevotella spp. (5-25%, depending on the diet), Roseburia spp. (5-10%), Eubacterium rectale (5-10%). The mucus layer is inhabited by mucus-degrading species such as Akkermansia muciniphila and Ruminococcus torques.

Major phyla and dominant species of the colonic microbiota in healthy adults

According to the results of the largest cohort studies (Human Microbiome Project-2. LifeLines-DEEP, Flemish Gut Flora Project II) from 2020-2025, the following phyla dominate the colonic microbiota of healthy people aged 18-65:

Phylum Firmicutes (53-75%): The families Ruminococcaceae and Lachnospiraceae have the largest share. The most important species are Faecalibacterium prausnitzii (with the strongest anti-inflammatory effect, number 1 butyrate producer), Subdoligranulum variabile, Ruminococcus bromii (starch fermenter), Roseburia intestinalis, R. inulinivorans, Eubacterium rectale, E. hallii, Coprococcus comes, Blautia wexlerae.

Bacteroidetes phylum (20-40%): families Bacteroidaceae, Prevotellaceae, Rikenellaceae. Main species: Bacteroides thetaiotaomicron, B. vulgatus, B. uniformis, B. ovatus, B. fragilis, Prevotella copri (decreased in diets high in animal protein and fat), Alistipes putredinis, Parabacteroides distasonis. Actinobacteria phylum (3-12%): B. longum, B. adolescentis, B. bifidum, B. pseudocatenulatum species of the genus Bifidobacterium are most common in adults. Verrucomicrobia phylum (0.5-5 %): Akkermansia muciniphila is the only representative that ferments mucus glycoproteins, and is sharply reduced in obesity, diabetes, and inflammatory diseases. The phylum Proteobacteria is usually less than 1%, but can increase to 10-50% in dysbiosis. The most common are: Sutterella wadsworthensis, Bilophila wadsworthia. Desulfovibrio spp. Among the archaea, Methanobrevibacter smithii is the most common, converting hydrogen gas into methane, increasing fermentation efficiency.

Microbiota stability and the concept of "core microbiota"

Individual microbiota, after stabilizing at 2-3 years of age, remains highly stable throughout life (0.75-0.92 according to the Jaccard index). At the same time, daily changes can reach 30-40% (especially depending on diet). but return to their original state within 2-4 weeks (resilience). The most stable are the Faecalibacterium, Roseburia, Bacteroides and Akkermansia species. The loss or 10-fold reduction of species included in the core microbiota is an early sign of many chronic diseases. For example, when Faecalibacterium prausnitzii is $<3\%$, the risk of

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inflammatory bowel disease increases 4-6 times, and when Akkermansia muciniphila is <0.1%, the likelihood of insulin resistance and obesity is 3-5 times higher. Thus, the preservation of the core microbiota is considered one of the most reliable biomarkers of overall health.

Physiological functions of normal microflora

The normal gastrointestinal microflora is a genetically and metabolically highly active "superorgan" that directly participates in almost all vital processes of the human body. Its functions are so numerous and profound that they can be divided into the following seven main areas: colonization resistance, short-chain fatty acid (SCFA) production and energy-metabolic regulation, formation of the mucosal immune system and constant immunomodulation, synthesis of vitamins and other bioactive substances, strengthening of the epithelial barrier function, neuroendocrine signaling and brain-gut communication. effects on the central nervous system through the axis, as well as the metabolism of xenobiotics and drugs. Colonization resistance is the oldest and most important defense mechanism of the microflora. A healthy microbiota prevents the colonization of pathogenic and opportunistic microorganisms in the intestine. This process is carried out through several parallel mechanisms. First, commensal bacteria (Bifidobacterium, Bacteroides, Faecalibacterium, Akkermansia) are the first to adhere to receptors in the glycocalyx and mucus layer of the intestinal epithelium, leaving no room for pathogens. Second, they produce bacteriocins, colicins, microcins, lantibiotics and other antimicrobial peptides (for example, Lactobacillus salivarius ABP-118, Enterococcus faecium enterosin AS-48, Bacillus subtilis subtilin). Third, anaerobic commensals rapidly consume oxygen and hydrogen, leaving no conditions for the growth of aerobic facultative anaerobic pathogens (Salmonella, Shigella, Campylobacter, pathogenic E. coli, Vibrio cholerae). Fourth, SCFA (especially butyrate and propionate) lower the pH to 5.5-6.7, blocking the sporulation and vegetative growth of Clostridium difficile, Listeria monocytogenes and other acid-sensitive pathogens. Fifth, species such as Bacteroides fragilis and Faecalibacterium prausnitzii degrade pathogen virulence factors (toxins, adhesins) through proteolytic enzymes. Recent studies have shown that Faecalibacterium prausnitzii alone secretes inhibitory substances against 217 pathogenic strains, including MAM (microbial anti-inflammatory molecule) that prevents inflammation. And Short-chain fatty acids (SCFA) acetate (C2), propionate (C3), butyrate (C4) and to a lesser extent isobutyrate, valerianate, isovalerianate are the most important metabolites of the intestinal microflora, which are formed as a result of anaerobic fermentation of dietary fibers, resistant starch, inulin, oligofructose and mucus glycoproteins. An average of 400-600 mmol of SCFA is produced per day, 95% of which is absorbed from the intestinal wall. Butyrate provides 60-70% of the energy of colonocytes of the large intestine, it penetrates the cell, inhibits histone deacetylases (HDAC1, HDAC3), increases the expression of p21, p27, Bax genes, as a result of which it prevents apoptosis and regulates proliferation. Butyrate binds to GLP-1 in L-cells through GPR41, GPR43 and GPR109A receptors. It increases the secretion of PYY and oxyntomodulin by 3-8 times, which improves insulin sensitivity, reduces glucagon secretion and reduces appetite. Propionate reduces gluconeogenesis (represses PEPCK and G6Pase genes) and cholesterol synthesis (inhibits HMG-CoA reductase) in the liver and peripheral tissues. Acetate, on the other hand, passes into the blood and activates POMC neurons in the hypothalamus, exerting an anorexigenic effect. Akkermansia muciniphila, Faecalibacterium prausnitzii, Roseburia intestinalis, Eubacterium rectale and Anaerostipes hadrus are the most potent butyrate producers, synthesizing 18-25 mmol of butyrate per 1 g of their cells.

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The formation and constant regulation of the mucosal immune system is the most complex function of the microflora. During the first 1000 days after birth, microbiota antigens initiate the differentiation of Treg. Th17 and IgA-producing B cells through dendritic cells, M-cells and Paneth cells. Faecalibacterium prausnitzii increases Foxp3 expression through butyrate and MAM, and increases IL-10 and TGF-β cytokines by 5-7 times. Clostridium cluster IV, XIVa and XVIII (Lachnospiraceae, Ruminococcaceae) species maintain the Treg/Th17 balance through SCFA. Akkermansia muciniphila increases the thickness of the mucus layer to 30-50 μm and stimulates M2-macrophage differentiation through GPR120. Bifidobacterium infantis, B. longurn and Lactobacillus rhamnosus GG modulate the NF-κB pathway via TLR-2, TLR-9 and NOD2 receptors, reducing pro-inflammatory cytokines (TNF-α, IL-6, IL-1B, IL-8). Secretory IgA is produced at 3-5 g per day, which neutralizes pathogens and food allergens. Germ-free animals have an 80-95% reduction in Peyer's patches, lymphocytes in the lamina propria and IgA+ plasma cells. In terms of vitamin and bioactive substance synthesis, microflora synthesizes vitamin K (menaquinone-4, MK-7, MK-9), B1 (thiamine), B2 (riboflavin), B3 (niacin), B5 (pantothenate), B6 (pyridoxine, pyridoxamine), B7 (biotin), B9 (folate), B12 (cobalamin) and other coenzymes. Bifidobacterium and Propionibacterium species are the main producers of B vitamins. Bacteroides fragilis and Eubacterium lentum play a leading role in the synthesis of vitamin K. 100-200 mcg of vitamin K and 20-50 mcg of B12 are synthesized in the intestine per day, which can be 2-5 times more than the amount obtained from food.

Epithelial barrier function is enhanced by butyrate, propionate, and Akkermansia muciniphila, which increases the expression of MUC2 and TFF3 genes, thickening the mucus layer by 2-3 times. The expression of zonula occludens-1 (ZO-1), occludin, and claudins increases, and tight junctions are strengthened. Butyrate activates the AMPK pathway, increasing cellular energy and preventing apoptosis. The effect through the gut-brain axis is one of the most surprising functions. The microbiota synthesizes 90% of serotonin (Lactobacillus, Streptococcus, Escherichia), GABA (Bifidobacterium, Lactobacillus), dopamine and noradrenaline precursors, as well as histamine and acetylcholine. Through the vagus nerve and through the blood (SCFAs, cytokines), the activity of the hypothalamus, amygdala and prefrontal cortex is altered. Lactobacillus rhamnosus JB-1 reduces depression and anxiety, Bifidobacterium longum 1714 improves cognitive function. In terms of xenobiotics and drug metabolism, Bacteroides, Eubacterium, and Clostridium species modify the activity of more than 50 drugs (digoxin, irinotecan, paracetamol, metformin). This is one of the main reasons for the individual response. In conclusion, normal microflora is an integral part of human physiology. Each of its functions is essential for life and is closely interconnected. Its disruption is the main cause of many chronic diseases.

Changes in age, lifestyle, and pathological conditions

The composition and functional state of the gastrointestinal microflora undergo dynamic changes throughout life. These changes occur under the influence of age-related physiological processes, dietary habits, geographical environment, lifestyle, drug intake (especially antibiotics), stress, and various pathological conditions. Large cohort studies over the past 10-15 years (Human Microbiome Project, LifeLines-DEEP, TwinsUK, American Gut, MyNewGut, Flemish Gut Flora Project, TEDDY) have revealed these dynamics in detail.

1. Neonatal period and early childhood (0-3 years)

The method of birth is crucial for the initial formation of the microbiota. In natural-born infants, Lactobacillus, Prevotella, Sneathia, Bifidobacterium species predominate from the first days, since they have the first contact with the maternal vaginal microbiota (Lactobacillus dominant) and skin microflora. In those born by cesarean section, Staphylococcus, Corynebacterium, Propionibacterium, Streptococcus and Enterobacteriaceae (especially Klebsiella, Enterobacter) are more abundant. This difference persists until 1 year of age and subsequently increases the risk of asthma, allergies, obesity by 1.5-3 times. During breastfeeding, Bifidobacterium longum subsp. infantis, B. breve, B. bifidum reach 70-90%, since these species can ferment human milk oligosaccharides (HMO) in breast milk. During artificial feeding, Bacteroides, Clostridium, Enterococcus and Lachnospiraceae increase. At 2-3 years of age, a composition close to that of adults is formed, but diversity is still low (Shannon index 2.5-3.5).

2. Childhood and adolescence (3-18 years old)

ratio 2-3:1 During this period, alpha diversity reaches its highest level (Shannon index 4.5-5.5). It stabilizes around Firmicutes/Bacteroidetes. Faecalibacterium prausnitzii, Akkermansia muciniphila, Roseburia spp. gradually increase. Enterotype Bacteroides predominates in Western countries, enterotype Prevotella in developing countries. Use of antibiotics 3-4 times a year (especially amoxicillin, macrolides) reduces diversity by 20-40%, and this effect lasts for 6-12 months.

3. Stable period of adults (18-65 years old)

During this period, the microbiota is most stable and resilient. At the individual "fingerprint" level, stability reaches 0.85-0.95. The core microbiota (Faecalibacterium, Bacteroides, Akkermansia, Roseburia, Eubacterium rectale) is present in more than 95% of people. Western diet (high protein, fat, refined carbohydrates) Bacteroides, Alistipes, Bilophila increase, while Mediterranean and plant-based diets increase Prevotella, Roseburia, Faecalibacterium. Regular alcohol consumption (>30 g/ethanol/day) decreases Bacteroidetes and increases Proteobacteria and Fusobacterium.

4. Old age (over 65 years old)

In old age, alpha diversity decreases by 15-30%, with the Firmicutes/Bacteroidetes ratio falling to 0.7-1.2. Faecalibacterium prausnitzii, Roseburia, Akkermansia muciniphila decrease by 30-70%, while Proteobacteria (Escherichia, Klebsiella, Enterobacter), Enterococcus, Staphylococcus and Clostridium cluster XI increase. These changes are associated with immunosenescence, sarcopenia, cognitive impairment and increased inflammation (inflammaging). Diversity is even lower in nursing home residents due to monotonous diet, low physical activity and frequent antibiotic use.

5. Lifestyle factors

Although an increase in Firmicutes and a decrease in Bacteroidetes were initially observed in obesity (BMI >30), recent meta-analyses found this difference to be not statistically significant. However, an increase in Christensenellaceae, Akkermansia, and Methanobrevibacter was associated with leanness, and an increase in Alistipes, Parabacteroides, and Bilophila was associated with obesity. Smoking increased Proteobacteria and Fusobacterium by 2-4 times.

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Physical activity (150 min of aerobic exercise per week) increased Roseburia, Faecalibacterium, and Lachnospira.

Sleep deprivation (≤6 hours) decreases Ruminococcaceae and increases Bacteroidaceae.

6. Effects of antibiotics and other drugs

Broad-spectrum antibiotics (cephalosporins, clindamycin, ciprofloxacin) reduce diversity by 30-70%, the effect lasts for 3-6 months (sometimes up to 2 years). The risk of Clostridium difficile infection increases 10-20 times. Proton pump inhibitors (omeprazole, pantoprazole) increase gastric pH, leading to an increase in Streptococcus, Enterococcus, Staphylococcus. Metformin increases Akkermansia and SCFA producers, which is part of its therapeutic effect.

7. Changes in pathological conditions

Inflammatory bowel disease (IBD, IBD): Faecalibacterium prausnitzii, Roseburia, Akkermansia, Eubacterium rectale are reduced by 50-90%, Proteobacteria (especially AIEC adherent-invasive E. coli), Fusobacterium nucleatum, Ruminococcus gnavus are increased. Irritable bowel syndrome (IBS): diversity decreases, Firmicutes/Bacteroidetes ratio is disrupted, Methanobrevibacter smithii (IIS-Q) or Bacteroidetes (IIS-D) predominate. Type 2 diabetes: Akkermansia muciniphila, Faecalibacterium prausnitzii, Roseburia intestinalis decrease, Betaproteobacteria, Escherichia increase. Depression and anxiety: Ruminococcaceae, Faecalibacterium decreases, Alistipes, Oscillibacter, Enterobacteriaceae increases. Autism spectrum disorder: Clostridium cluster I, III, XI, Desulfovibrio, Sutterella increase, Bifidobacterium, Prevotella decrease. Colorectal cancer: Fusobacterium nucleatum, Peptostreptococcus, Porphyromonas, Parvimonas, Bacteroides fragilis (enterotoxigenic strains) increase, butyrate producers decrease sharply.

8. Oncological processes and other diseases

In colorectal cancer, Fusobacterium nucleatum increases 10-100-fold, which activates E-cadherin through FAD adhesin and activates the Wnt/ß-catenin pathway. In liver cirrhosis and hepatocellular carcinoma, Enterobacteriaceae and Streptococcus increase, and SCFA producers decrease. In rheumatoid arthritis, Prevotella. copri is associated with an increase. In Parkinson's disease, Enterococcus, Lactobacillus increase, Faecalibacterium, Roseburia decrease. In Alzheimer's disease, Bacteroides, Alistipes increase, and Eubacterium rectale decrease.

In conclusion, any changes in the gastrointestinal microflora, whether age-related, lifestyle-related, or disease-related, reflect the overall state of human health. Early detection and correction of these changes is one of the most important tasks of modern medicine.

Modern approaches to microbiota modulation and future prospects

Targeted modulation of the microbiota has become one of the fastest growing therapeutic areas in the past 10 years. Methods currently in clinical practice and in the testing phase include: probiotics, prebiotics, synbiotics, postbiotics, fecal microbiota transplantation (FMT), next-generation probiotics, engineered bacteria, bacteriophages, microbiome-targeted diets, and personalized microbiome medicine. Probiotics are live microorganisms that, when administered in adequate amounts, confer a beneficial effect on the health of the macroorganism (FAO/WHO

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2002 definition). The best-studied strains are: Lactobacillus rhamnosus GG (LGG), Bifidobacterium animalis subsp. lactis BB-12, Bifidobacterium longum BB536, Saccharomyces boulardii CNCM 1-745, Lactobacillus reuteri DSM 17938, Lactobacillus casei Shirota, Escherichia coli Nissle 1917. They reduce the risk of antibiotic-associated diarrhea by 57% (RR 0.43; 95% CI 0.34-0.53), necrotizing enterocolitis by 50-60%, and nosocomial infections by 30-40%. Recent meta-analyses (Cochrane 2023, Lancet 2024) have shown that LGG and S. boulardii It is estimated to be 65-70% effective in preventing recurrent C. difficile infection (in combination with antibiotics).

trans-Prebiotics are nutrients that are not digested by human small intestinal enzymes, but are selectively fermented by beneficial bacteria in the colon. The best-proven ones are: inulin, fructooligosaccharides (FOS), galactooligosaccharides (GOS), galactooligosaccharides, lactulose, resistant starch (RS2. RS3), xylooligosaccharides (XOS). 5-15 g of prebiotic per day increases Bifidobacterium and Faecalibacterium by 1-2 logs, increases butyrate production by 30-80%. The combination of GOS and inulin brings bifidobacterial levels in infants closer to those in breast milk. Synbiotics are a targeted combination of probiotics and prebiotics that have a synergistic effect. For example, B. longum + inulin, L. rhamnosus GG + GOS, B. lactis BB-12 + GOS. In randomized studies, synbiotics reduce body weight by 1.5-3 kg and HbA1c by 0.4-0.7%. Postbiotics are non-living bacterial products or metabolites (cell wall fragments, SCFAs, bacteriocins, exopolysaccharides). They are potent immune modulators, have a high safety profile, and a long shelf life. For example, a heat-killed form of Lactobacillus rhamnosus GG or a microencapsulated form of butyrate are effective in prolonging remission in UTIs.

Fecal microbiota transplantation (FMT) is currently the most powerful modulating method. Its efficacy in recurrent and refractory Clostridium difficile infection is 90-95% (single procedure). According to the FDA and EMA for 2023-2025, standardized donor fecal preparations (RBX2660, SER-109) have a cure rate of 80-88%. Clinical remission rates of 40-50% in ulcerative colitis (randomized studies, 2024), 30-45% in Crohn's disease, and 35-60% in irritable bowel syndrome are shown. Currently, more than 120 clinical trials (Clinical Trials.gov, 2025) are studying FMT in obesity, type 2 diabetes, autism, depression, Parkinson's, Alzheimer's, metabolic syndrome, and even oncological diseases. A new direction is autologous FMT (storing and then reintroducing feces collected before the disease).

New generation probiotics (NGP) are, unlike traditional probiotics, species that occur naturally in the healthy human microbiota but have not been previously cultured: Akkermansia muciniphila (Pasteur Institute, 2022-2025 trials). Faecalibacterium. prausnitzii (4D Pharma), Anaerobutyricum (Roseburia) hallii, Christensenella minuta, Eubacterium hallii. Akkermansia muciniphila WST01 improves insulin sensitivity in obesity and diabetes by 25-40% (Phase II, 2025). Faecalibacterium prausnitzii A2-165 achieves remission in up to 65% of NCC. Engineered bacteria are genetically modified strains that produce targeted therapeutics. For example, Lactococcus lactis (AG013), which produces IL-10, is being used in oral administration and in NSCLC. A strain of E. coli Nissle 1917 that produces a GLP-1 analog is undergoing clinical trials in obesity. Bacteriophages are being used to eliminate targeted pathogens (Fusobacterium nucleatum, AIEC, Klebsiella). A personalized microbiome-focused diet is the safest and most cost-effective approach. Mediterranean diet, plant-based diet (≥30 plant species per week) increases alpha-diversity by 20-40%, SCFAs by 50-100%. Intermittent fasting (16/8) increases Akkermansia and Lactobacillus. Future prospects - personalized microbiome medicine. As of 2025, microbiome profiling (16S rRNA + shotgun metagenomics + metabolomics) has begun to be introduced into clinical practice, like a simple blood test. Machine learning. algorithms (Random Forest, Deep Learning) predict disease risk based on microbiome data with 85-95% accuracy. By 2030, each person will have a "microbiome passport", based on which individual probiotics, prebiotics, diets and even synthetic microbiota will be prepared.

In summary, microbiota modulation currently covers a wide spectrum, from simple probiotics to engineered bacteria and individual microbiome-based therapies. This direction is fundamentally changing not only gastroenterology, but also cardiology, endocrinology, neurology, psychiatry, oncology and immunology, leading medicine to a new microbiome-centric paradigm.

Summary

The normal microflora of the gastrointestinal tract is one of the most important physiological systems of the human body, which not only ensures the digestion and absorption of nutrients, but also forms the immune system, regulates metabolic processes, creates colonization resistance against pathogenic microorganisms, and directly affects the functioning of the central nervous system through the brain-gut axis. As a result of metagenomic studies in the last decade, it has been established that the colonic microbiota of a healthy person consists of 500-1000 species, of which 90-99% belong to the phyla Firmicutes and Bacteroidetes. The most important functional representatives Faecalibacterium prausnitzii, Akkermansia muciniphila, Roseburia intestinalis, Eubacterium rectale, Bacteroides thetaiotaomicron and Bifidobacterium longum are the main factors of macroorganism health by producing branched-chain fatty acids, vitamins, neurotransmitters and immune-modulating substances. short

Lifelong dynamics of the microbiota from the neonatal period to old age In modern medicine, effective methods of microbiota modulation include high-quality probiotics, prebiotics, synbiotics, postbiotics, standardized fecal microbiota transplantation, and new generation probiotics (Akkermansia muciniphila, Faecalibacterium prausnitzii) and are already being introduced into clinical practice. The effectiveness of FMT in recurrent Clostridium difficile infection has reached 90-95%, in ulcerative colitis 40-50%, and initial results in obesity and metabolic syndrome are promising. In the future, modulation of the microbiome based on individual genetic, metabolic, and clinical profiles, i.e., “personalized microbiome medicine,” will remain the most important strategic direction of medicine. By 2030, the preparation of individual probiotics, diet, and synthetic microbiota according to each patient’s “microbiome passport” will become common practice. Thus, the normal microflora of the gastrointestinal tract is an integral part of human health, and its disruption is the main cause of many modern diseases. Preservation, early diagnosis and targeted modulation of the microbiota are today the most important tasks not only for gastroenterology, but also for all areas of medicine.

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