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NORMAL HUMAN MICROBIOTA AND DYSBIOSIS: BIOLOGY, HEALTH EFFECTS, AND CLINICAL RELEVANCE

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Abstract: The human microbiota comprises diverse communities of bacteria, fungi, viruses, and archaea that colonize various body sites and play essential roles in maintaining health. These microorganisms contribute to metabolism, immune regulation, barrier integrity, and protection against pathogens. Advances in culture-independent techniques, including 16S rRNA sequencing and metagenomics, have significantly enhanced understanding of microbial diversity and function. Dysbiosis, defined as an imbalance in microbial composition or function, has been associated with numerous diseases, including inflammatory bowel disease, obesity, metabolic syndrome, allergic disorders, autoimmune diseases, and neuropsychiatric conditions. This review summarizes the composition and functions of normal human microbiota, mechanisms underlying dysbiosis, disease associations, and current therapeutic strategies targeting the microbiome.

Keywords: Microbiota, Microbiome, Dysbiosis, Gut Microbiota, Probiotics, Fecal Microbiota Transplantation

Introduction

The human body harbors trillions of microorganisms collectively known as the microbiota. Their combined genetic material, termed the microbiome, contributes significantly to host physiology and health (1,2). Recent advances in sequencing technologies have revealed that healthy individuals possess highly diverse microbial communities that vary by anatomical site while maintaining important functional roles (1–3). Alterations in these microbial ecosystems, known as dysbiosis, have been increasingly implicated in the pathogenesis of multiple diseases.

Normal Human Microbiota:

Gastrointestinal Tract

The gastrointestinal tract contains the largest microbial population in the human body. The colon is predominantly populated by anaerobic bacteria belonging to the phyla Firmicutes and Bacteroidetes, along with Actinobacteria and Proteobacteria (3,4). Gut microbiota contribute to digestion, vitamin synthesis, short-chain fatty acid (SCFA) production, immune regulation, and protection against pathogens (5).

Skin Microbiota

The skin hosts diverse microbial communities influenced by moisture, temperature, and sebum production. Common microorganisms include Staphylococcus epidermidis, Cutibacterium acnes, and Corynebacterium species (6). These organisms support skin barrier function and inhibit colonization by pathogenic microbes.

Oral Microbiota

The oral cavity contains one of the most diverse microbial ecosystems in the body. Dominant genera include Streptococcus, Actinomyces, Veillonella, and Prevotella (7). Disruption of oral microbial balance contributes to dental caries and periodontal disease.

Respiratory, Vaginal, and Urinary Microbiota

The respiratory tract harbors distinct microbial communities that influence respiratory health (8). In reproductive-age women, Lactobacillus species dominate the vaginal microbiota and maintain an acidic environment that protects against infections (9). Emerging evidence also supports the existence of resident microbiota within the urinary tract (10).

Factors Influencing Microbiota Composition

Several factors shape microbial composition throughout life, including:

- Mode of birth delivery
- Infant feeding practices
- Diet and nutrition
- Age and hormonal status
- Antibiotic exposure
- Environmental and geographical factors
- Chronic diseases and immune status (1,3,5)

Early-life microbial colonization is particularly important for immune system development and long-term health outcomes.

Dysbiosis: Definition and Mechanisms

Dysbiosis refers to alterations in microbial composition, diversity, or function associated with disease states (11). Common features include:

- Loss of beneficial microorganisms
- Expansion of pathogenic or opportunistic species
- Reduced microbial diversity
- Altered metabolic activity

Microbial dysbiosis can impair epithelial barrier function, disrupt immune regulation, alter metabolic pathways, and promote chronic inflammation (12).

Disease Associations

Gastrointestinal Diseases

Inflammatory bowel disease (IBD) is strongly associated with reduced microbial diversity and depletion of beneficial SCFA-producing bacteria such as Faecalibacterium prausnitzii (13).

Dysbiosis also contributes to Clostridioides difficile infection and may play a role in irritable bowel syndrome.

Metabolic Disorders

Gut microbiota influence energy harvest, lipid metabolism, and insulin sensitivity. Altered microbial profiles have been linked to obesity, type 2 diabetes mellitus, and non-alcoholic fatty liver disease (14).

Allergic and Autoimmune Diseases

Reduced microbial diversity during early life may contribute to abnormal immune development, increasing susceptibility to asthma, eczema, food allergies, and autoimmune diseases (15).

Neuropsychiatric Disorders

The gut-brain axis facilitates communication between intestinal microbiota and the central nervous system through neural, endocrine, immune, and metabolic pathways. Dysbiosis has been associated with depression, anxiety, and autism spectrum disorders, although causal relationships remain under investigation (5).

Therapeutic Approaches

Probiotics and Prebiotics

Probiotics are live microorganisms that confer health benefits when administered in adequate amounts, while prebiotics selectively stimulate beneficial microbial growth. Evidence supports their use in selected gastrointestinal disorders and prevention of antibiotic-associated diarrhea (5).

Fecal Microbiota Transplantation

Fecal microbiota transplantation (FMT) has emerged as a highly effective treatment for recurrent Clostridioides difficile infection. Research is ongoing regarding its role in IBD and metabolic disorders (5).

Dietary Interventions

Diet remains one of the most effective tools for microbiome modulation. High-fiber, plant-based diets promote microbial diversity and SCFA production, whereas highly processed diets are associated with dysbiosis (5).

Challenges and Future Directions

Despite substantial progress, several challenges remain. Many microbiome studies are observational, limiting causal inference. Variability in sampling methods, sequencing technologies,

and analytical approaches can affect study reproducibility. Future research should focus on standardized methodologies, longitudinal studies, and personalized microbiome-based therapies (3,11).

Conclusion

The human microbiota is an essential component of health, influencing metabolism, immunity, and resistance to infection. Dysbiosis has been implicated in numerous gastrointestinal, metabolic, allergic, autoimmune, and neuropsychiatric disorders. Continued advances in microbiome research are expected to improve disease prevention, diagnosis, and treatment through targeted microbiota-based interventions.

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