



THE MICROBIOME

We define the microbiome as the community or ecosystem of microorganisms, such as bacteria, fungi, and viruses, that live in and on your body. We live in synergy with healthy microorganisms. These trillions of organisms are one of the first lines of defenses against illness. These microorganisms can help with digestion of complex starches, some vitamin production, and even help to educate the adaptive part of our immune systems.

Most of your microbiome is in your gut, which includes your mouth, throat, stomach, and intestines. Other environments on your body include the integument, (skin, respiratory tract, gut and urogenital) as well. Your microbiome can contain both beneficial and harmful microorganisms which affects your health and well-being. To this end within the GI tract, skin and urogenital region there exists a highly dynamic microbial environment that harbors many distinct substrata and microenvironments that house diverse microbial communities. *The composition of the microbiome is shaped throughout life by factors including host genetics, maternal-fetal transmission, as well as environmental factors, such as dietary habits, hygiene practices, medications, and systemic factors. This dynamic ecosystem presents opportunities for oral microbial dysbiosis and the development of various diseases. The application of both in vitro and culture-independent approaches has broadened the mechanistic understandings of complex polymicrobial communities within the body, as well as the environmental, local, and systemic underpinnings that influence the dynamics of the microbiome.

The list of microorganisms is too long for the purposes of this handout, but in summary, following birth, overt colonization of the oral cavity and skin with microbes occurs within 8-16 hours as a result of transmission of microbes vertically (through exposure to maternal skin and vaginal microbiomes), from the diet via oral fixation by the infant, and horizontally (from human interactions additional to those already mentioned). The infant mouth becomes colonized by early oral colonizers associated with the infant's mode of delivery, demonstrated by finding distinct differences in the bacterial phyla predominant in the oral cavities of babies delivered vaginally compared with those delivered by Cesarean section. Firmicutes, Bacteroides, and Actinobacteria were found to be most abundant, respectively, in babies delivered vaginally, while Bacteroides, Proteobacteria, and Firmicutes were most abundant in babies delivered by Cesarean section. Regarding mode of delivery, vast differences in relative abundance at the genus level have been observed for most phyla, with the most marked increases being observed for *Lactobacillus* species in children delivered vaginally and for *Petrimonas* species in children delivered by Cesarean section. *Lactobacillus* species are common constituents of the vaginal microbiome, with strong consistency found between lactobacilli in the microbiota of the vagina and those in the oral cavity of infants delivered vaginally after natural labor and birth.

The infographic features a central illustration of the human digestive system, including the stomach, small intestine, and large intestine. A label 'Human intestine' points to the large intestine. To the left, under the heading 'Beneficial bacteria', are three circular images of bacteria: yellow rod-shaped *Bifidobacteria*, blue rod-shaped *Escherichia coli*, and blue spherical *Lactobacilli*. To the right, under the heading 'Harmful bacteria', are three circular images: purple rod-shaped *Campylobacter*, purple rod-shaped *Clostridium difficile*, and purple spherical *Enterococcus faecalis*. A label 'Beneficial bacteria isolated from stool sample for FMT' points to a sample of stool in the large intestine.

Beneficial bacteria

Bifidobacteria
Various strains help to modulate immune responses, regulate other gut bacteria, prevent tumour formation, and produce vitamins.

Escherichia coli
Various strains help to produce vitamin K2 (important to blood clotting), keep bad bacteria in check. Some strains can cause disease.

Lactobacilli
Beneficial varieties produce vitamins and nutrients, boost immunity and protects against carcinogens.

Harmful bacteria

Campylobacter
C. jejunii and *C. coli* strains most commonly associated with human disease. Usually ingested through contaminated food.

Clostridium difficile
Most dangerous when it proliferates following a course of antibiotics.

Enterococcus faecalis
Common cause of post-surgical infections

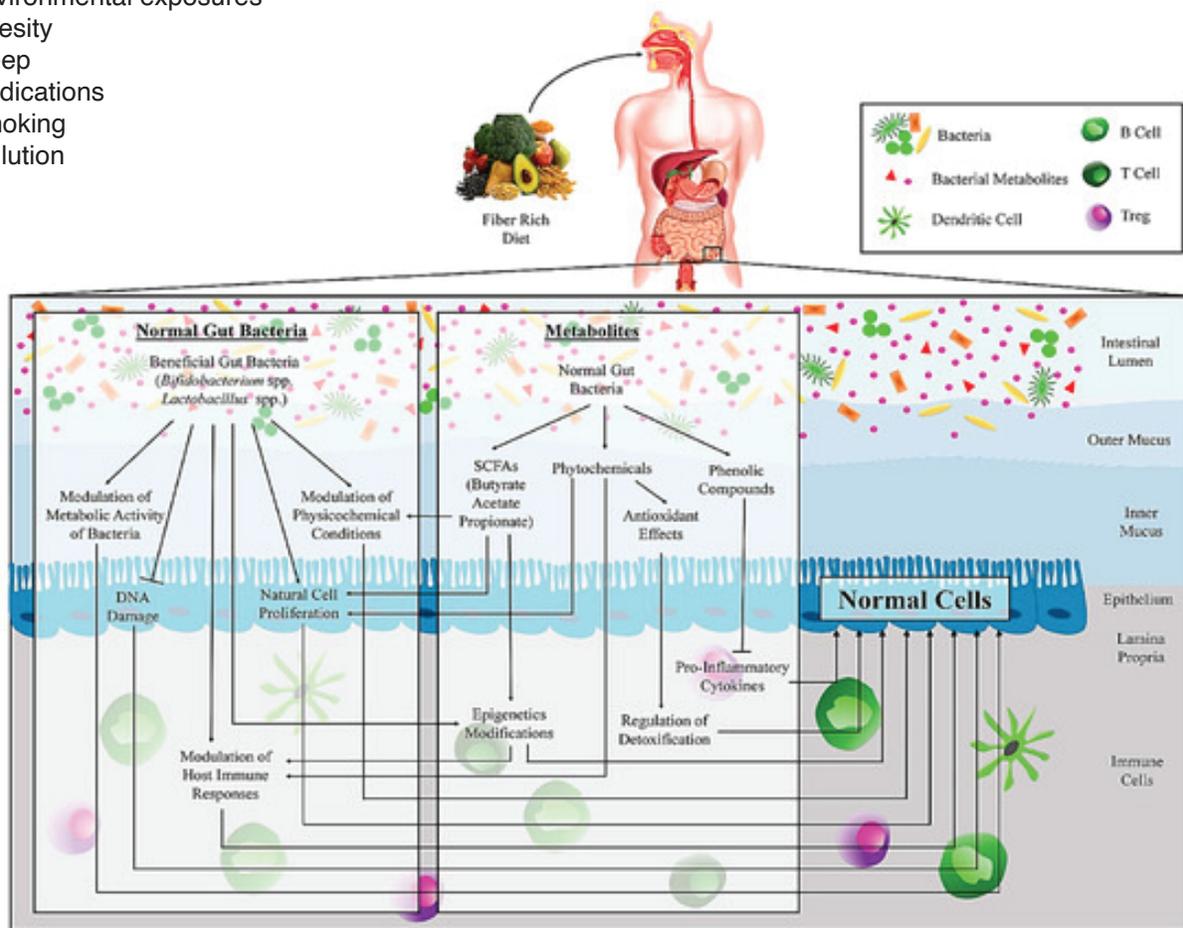
Human intestine

Beneficial bacteria isolated from stool sample for FMT

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Factors that can affect the microbiome include:

- Diet: What we eat has a great effect on our gut bacteria.
- Stress: Stress can disturb gut microbiota, and this can, in turn, cause various disorders and diseases.
- Exercise: Exercise may increase the number of 'good' bacteria and enrich gut microbial diversity.
- Microbial metabolites, e.g. short-chain fatty acids affect gut–brain signaling and the immune response.
- Gastric Bypass Surgery
- Environmental exposures
- Obesity
- Sleep
- Medications
- Smoking
- Pollution



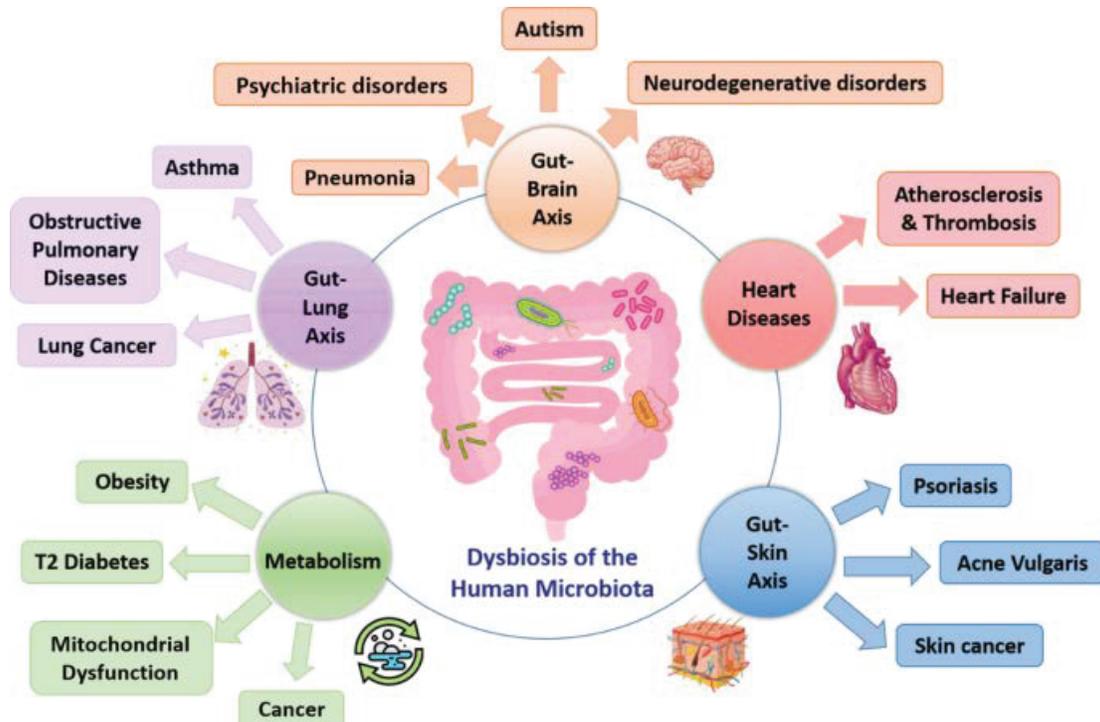
The gut microbiome, i.e., the community of bacteria and other microorganisms living in the human gut, has been implicated both directly and indirectly (mediating the effects of diet) on human health. The associations between gut microbiome composition and disease status have been widely reported, while recent studies have demonstrated a role for the gut microbiome in influencing remote organs, mucosal, and immune function. Considerable effort is currently focused on understanding the natural history of microbiome development in humans in the context of health outcomes, in parallel with improving our knowledge of microbiome–host molecular interactions. These efforts ultimately aim to develop effective approaches to rehabilitate perturbed human microbial ecosystems to restore health and prevent disease.

Differences in gut microbiome composition and function have been associated with a variety of chronic diseases ranging from gastrointestinal inflammatory and metabolic conditions to neurological, cardiovascular, and respiratory illnesses.



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Below is a of causal links that are associated with various perturbations in the microbiome. It is postulated that these alterations in flora can aid in or lead to various conditions.



TREATMENT

Microbiome therapeutics are aimed at engineering the microbiome using additive, subtractive, or modulatory therapy with an application using native or engineered microbes, antibiotics bacteriophages, and bacteriocins. This approach could overcome the limitation of conventional therapeutics by providing personalized, harmonized, and sustainable treatment.

Most Common microorganisms in the gut:

- A. Firmicutes – breakdown carbohydrates in the gut that cannot be digested by the body's enzymes such as dietary fiber and resistant starches.

Some Examples:

1. Lactobacillus
2. Bacillus

- B. Bacteroidetes - many species that live in synergy in our guts but are virulent when they escape the gut. These organisms provide protection from pathogens and provide nutrients to other microbials in the gut.

Some Examples:

1. Bacteroides fragilis
2. Bacteroides thetaiotaomicron
3. Bacteroides vulgatus



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TREATMENT continued

C. Actinobacteria - Actinobacteria phylum (includes several species), despite it representing a minority group of commensal bacteria, plays a pivotal role in the development and maintenance of gut homeostasis. Its involvement has been supposed in the modulation of gut permeability, immune system, metabolism, and gut-brain axis.

Some Examples:

1. Streptomyces
2. Corynebacterium
3. Mycobacterium

D. Proteobacteria - increasing amount of data identifies Proteobacteria as a possible microbial signature of disease. Several studies demonstrate an increased abundance of members belonging to this phylum in such conditions. Major evidence currently involves metabolic disorders and inflammatory bowel disease. However, more recent studies suggest a role also in lung diseases, such as asthma and chronic obstructive pulmonary disease, but evidence is still scant. Notably, all these conditions are sustained by various degree of inflammation, which thus represents a core aspect of Proteobacteria-related diseases.

Some Examples:

1. E. Coli
2. Salmonella
3. Yersinia
4. Legionella
5. Vibrio

E. Fusobacteria – activate host responses designed to protect against pathogens that promote tumor growth.

Some Examples:

1. Fusobacterium nucleatum
2. Fusobacterium necrophorum

F. Verrucomicrobia - has anti-inflammatory properties that further aid in intestinal health and glucose metabolism.

Some Examples:

1. Verrucomicrobium spinosum
2. Prosthecobacter dejongeii
3. Chthoniobacter flavus

The microbiome is very complex with research ongoing to help us better understand the associated conditions leading to health and dysbiosis. The above is merely an introduction to this expansive subject.

Once we meet and determine your specific needs, we can better understand how this may impact your overall health and wellbeing.
