UDC 664:636.085.55:[612.3:591.13]

MICROBIOMES OF HUMAN, LIVESTOCK ANIMAL GASTROINTESTINAL TRACT, FOOD PRODUCTS AND COMPOUND FEEDS: CONNECTIONS AND IMPACTS. PART 2

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https://doi.org/10.15673/fst.v18i1.2790

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Cite as Vancouver style citation

Iegorov B, Iegorova A, Yeryganov K. Microbiomes of human, livestock animal gastrointestinal tract, food products and compound feeds: connections and impacts. Part 2. Food Science and Technology. 2024;18(1):4-14. https://doi.org/10.15673/fst.v18i1.2790

Цитування згідно ДСТУ 8302:2015

Iegorov B., Iegorova A., Yeryganov K. Microbiomes of human, livestock animal gastrointestinal tract, food products and compound feeds: connections and impacts. Part 2 // Food Science and Technology. 2024. Vol. 18, Issue 1. P. 4-14. https://doi.org/ 10.15673/fst.v18i1.2790

Abstract. Research on the human gut microbiome began long ago and currently uses the latest modern methods and creates new insights and understanding. The human gut microbiome contains billions of microbial cells per 1 g of intestinal contents. These microbes include members of all superkingdoms: prokaryotes (kingdoms Bacteria and Archaea), eukaryotes (Fungi), and viruses. The taxonomic composition includes hundreds of bacterial species, dozens of archaeal and fungal species, and dozens of viral families. They are constantly in close connection and interaction with each other and with host cells and tissues. Methanogenic archaea have been shown to potentially impact the development of certain diseases, and fungi and bacteria are beneficial symbionts that have a significant impact on host health. Viruses are mostly bacteriophages that modulate bacterial populations. The impact on human health occurs through complex molecular mechanisms: microbes secrete biologically active metabolites that modulate cellular and tissue biochemical activity and, hence, the functioning of the immune system and other organs, including the CNS. In turn, the human body responds using its nervous and immune systems and local intestinal tissues that produce certain substances that modify the activity of microorganisms. This results in formation of a gut-brain axis consisting of afferent (to the brain) and efferent (from the brain) pathways. A correlation between the composition of the microbiota and the development of some intestinal and non-intestinal diseases, including neurodegenerative and behavioral disorders, has been shown. The human gut microbiota varies throughout a person's life, and differs significantly by age (from infancy to the elderly) in terms of the taxonomic proportions. At the same time, food products contain hundreds of species of microbes, i. e. various bacteria and fungi (yeast and mycelial). This food microbiota can have an impact on the gut microbiota, especially in children (infants, preschool) and elderly. However, this issue has not been investigated and should be studied in the future.

Keywords: microbiome, gastrointestinal tract, microecology, gut-brain axis, immune response, food products.

Introduction. Formulation of the problem

To date, a great deal of knowledge has been accumulated about the normal microbiota of the human gastrointestinal tract (GIT). It is well known that this microbiota consists of billions of bacterial cells belonging to many dozens of genera and hundreds of species, as well as non-bacterial microorganisms (archaea) or agents (viruses).

Similarly, a lot of information has been accumulated on the microbiota of food products, divided into different categories (manufacturing microbiota, spoilage microbiota, opportunistic or obligate pathogens). Under certain conditions (permissible content exceeded, certain species or strains present), this microbiota makes food unfit for consumption, both because of spoilage and the risk of poisoning, and because of the risk of foodborne infection.

At the same time, the impact of the food microbiota (without the presence of pathogenic species or strains and with a normal, unspoiled condition of the product) on the normal human gastrointestinal microbiota has not been studied and has to be revealed.

The objective of this review was to summarize the knowledge of the human gut microbiome, its role in human physiology and health, and the food microbiota and its impact on human health, highlighting areas that could be investigated in the future.

The purpose of this study was to assess the current knowledge about the microbiomes of the human gastrointestinal tract and food products.

To achieve this goal, the following **tasks** were set:

1) to review the literature on human gut and food microbiomes and the role of the gut microbiome in human health;

2) to highlight unresolved issues for further research and development.

1. Human GIT microbiome

The human GIT microbiome consists of representatives of three groups of organisms:

1) superkingdom Procaryota – kingdoms Bacteria and Archaea;

2) superkingdom Eukaryota – kigdom Fungi;

3) viruses.

Microorganisms are found in the intestinal contents in huge quantities (Fig. 1) [1].

The figure shows that bacteria are the most abundant group (up to 1012 cells per 1 g of intestinal content), although the number of viruses and archaea is not much inferior to them (up to 1010 per 1 g of intestinal content), and the number of fungi is much lower (up to 106 per 1 g).

The microbiota in the human intestine appears very quickly after birth: its first representatives come from the mother's birth canal, then it begins to enter with food, and during the first decade of life, under the influence of dietary changes, the intestinal microbiome develops to a more mature state [2, 3, 4].

1.1. Bacteria

According to the study [5], 461 existing species and 368 potential species (based on metagenomic and metataxonomic studies), as well as 416 potential taxa of superspecies ranks were identified. The existing 461 species include representatives of 198 genera in 10 phyla, the 368 potential species include 130 genera in 8 phyla, and the 416 superspecies taxa include 60 genera in 3 phyla. The researchers grouped all these species and other taxa into 1235 species-level phylotypes, i.e. morphologically and biochemically similar species, which potentially reflects their common evolution in the gut microbiome in the past.

Fig. 2 shows a diagram of proportional relationships between the main phylotypes according to the same study [5]. A proportional relationship means that the phylotypes have proportional abundances of genetic markers. In the figure, pink lines indicate a direct proportionality, and green lines indicate an inverse proportionality.

In addition, not all taxa of microorganisms inhabiting the intestine are known to be equally active in biochemical processes aimed at maintaining microbiome homeostasis. Therefore, they make different contributions to it. Thus, the authors of the study [6] used the amount of RNA as an indicator of cell activity (intensive RNA synthesis indicates high metabolic activity and cell proliferation), the results of their study are shown in Fig. 3.

This indicates significant differences in the contribution of different groups of microorganisms to the functioning of the intestinal microbiome. Some phyla (groups) can be seen to be very abundantly represented in the active part of the microbiome, while others are almost absent there at all.

There is a considerable number of studies of the age-related dynamics of the gastrointestinal microbiome from infancy to old age. For example, the results of the study [7] are shown in Fig. 4.

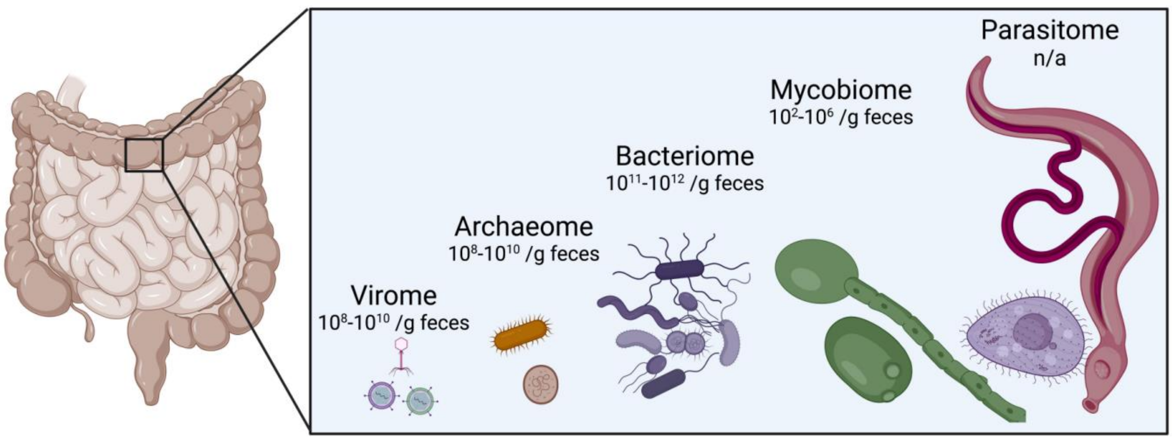


Fig. 1. Comparison of the number of different groups of microorganisms in the human colon [1]

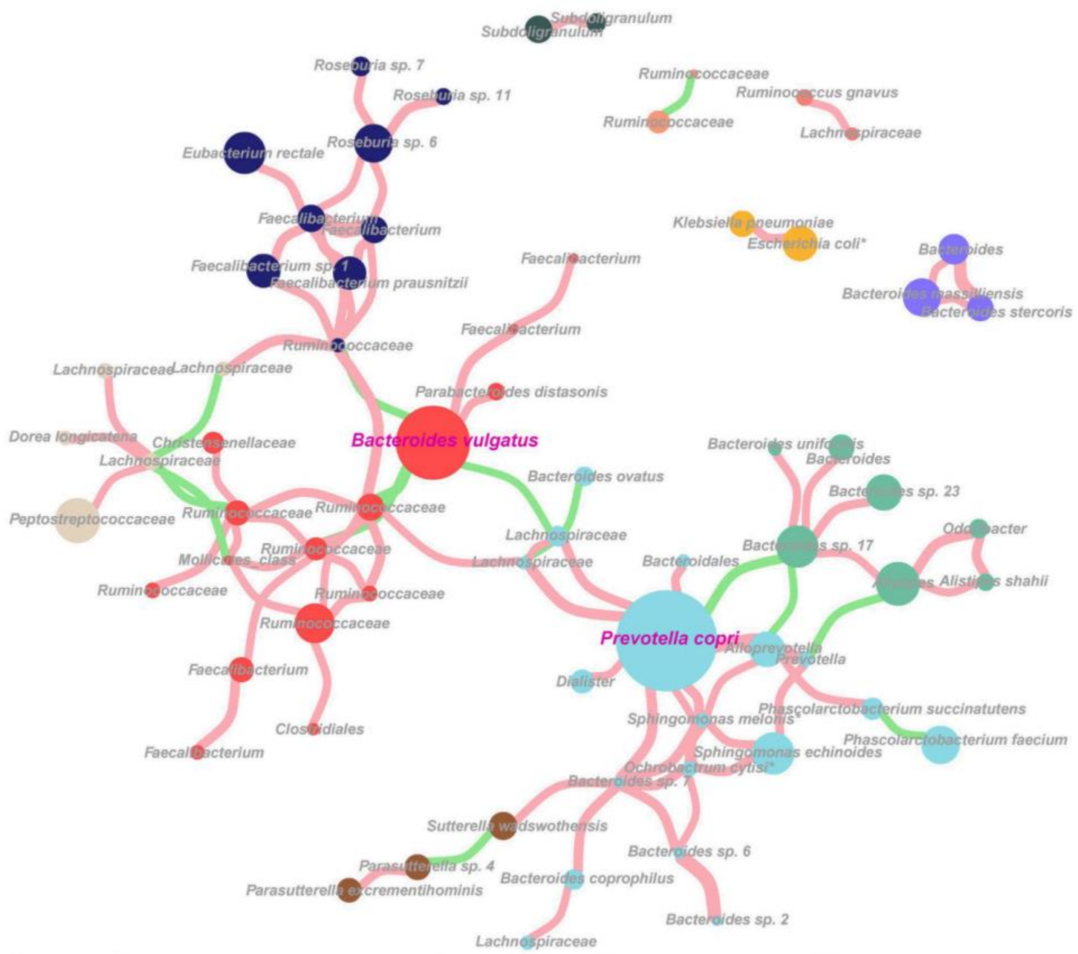


Fig. 2. Proportional relationships between the main bacterial phylotypes in the human intestinal microbiome according to the study [5]

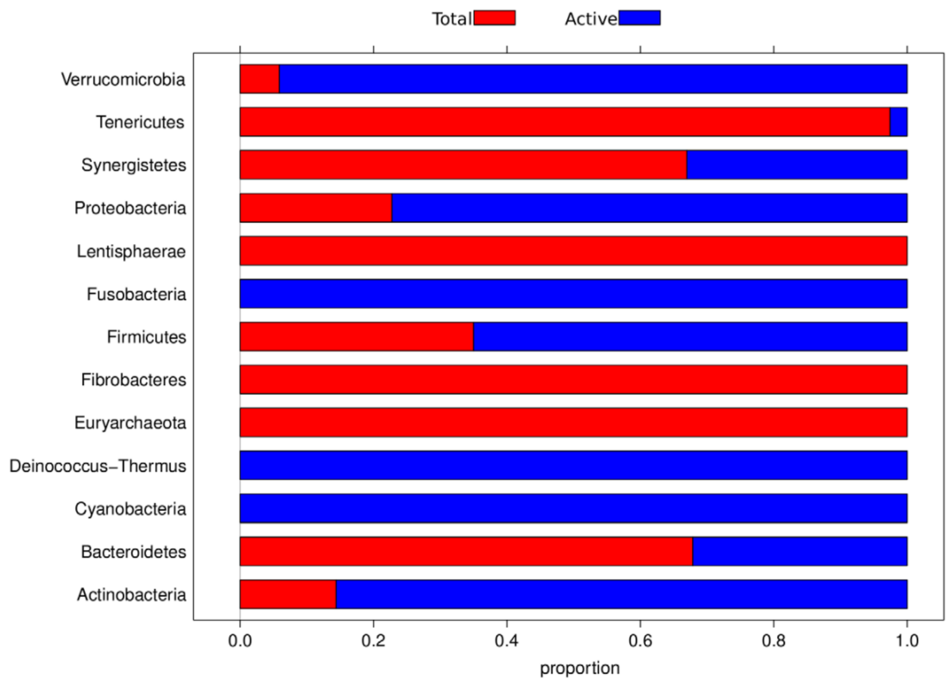
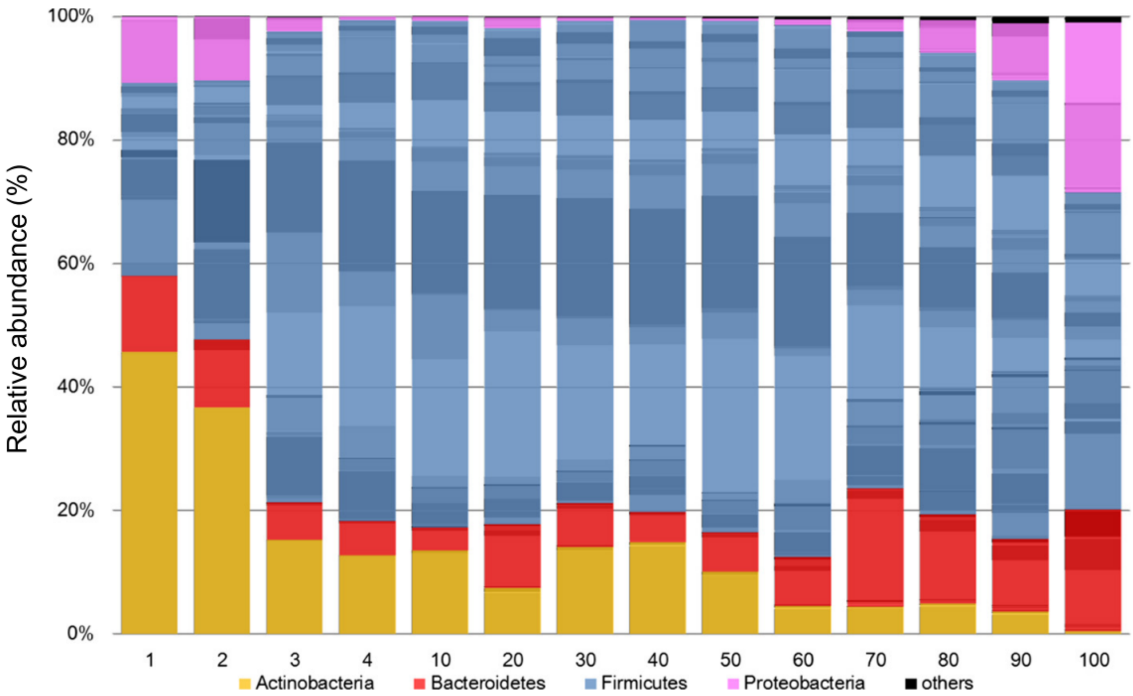


Fig. 3. Fractions of phyla in the total microbiome and its active part according to the study [6]



1 – milk feeding, 2 – supplementary feeding, 3 – complete weaning, 4 – between 4 and 9 years, subsequent numbers – segments of 9 years to the next point (10-19, 20-29, etc.)

Fig. 4. Age-related changes in the human gastrointestinal microbiota (phyla) according to [7]

The figure shows that *Proteobacteria* (gram-negative rods) had the highest abundance, and this does not change with age. *Firmicutes* are the second most abundant bacteria, and the contribution of this group decreased at the end of life. The content of *Bacteroidetes* (gram-negative anaerobes) also decreased, and the content of actinobacteria fell from almost 50% to almost 0%. The *Proteobacteria* phylum includes the *Enterobacteriaceae* family, as well as pseudomonads, campylobacters, and vibrios. The gram-positive *Firmicutes* phylum includes two common spore-forming genera, *Bacillus* and *Clostridium*, as well as lactobacilli and gram-positive cocci (in particular, staphylococci, streptococci, and enterococci). The *Bacteroidetes* phylum includes, among others, the widespread genera *Bacteroides*, *Prevotella*, *Flavobacterium*, *Porphyromonas*. The *Actinobacteria* phylum includes, among others, bifidobacteria and mycobacteria [7].

Other studies confirm this picture. Table 1 shows data from a study [8] on the main groups of bacteria in the human gastrointestinal tract.

As can be seen from the table, the greatest diversity in the human gastrointestinal tract is demonstrated by representatives of the *Firmicutes* phylum – gram-positive rods, including spore-forming, and cocci. This phylum includes lactic acid rods (lactobacilli), clostridia, and streptococci. The second place is held by representatives of the *Bacteroidetes* phylum - gram-negative obligate anaerobic rods. The *Actinobacteria* and *Proteobacteria* phyla are represented by only one major genus each: bifidobacteria and *Escherichia*, respectively.

Table 1 – The most important groups of bacteria in the human gastrointestinal tract according to [8]

Phylum	Family	Genus
Actinobacteria	*Bifidobacteriaceae*	*Bifidobacterium*
Bacteroidetes	*Bacteroidaceae*	*Bacteroides*
	Porphyromonadaceae	*Parabacteroides*
	Prevotellaceae	*Prevotella*
	Rikencellaceae	*Alistipes*
Firmicutes	*Clostridiaceae*	*Clostridium*
	Eubacteriaceae	*Eubacterium*
	Erysipelotrichaceae	*Erysipelatoclostridium*
	Lachnospiraceae	*Blautia*
		Coprococcus
		Dorea
		Lachnoclostridium
		Roseburia
	Lactobacillaceae	*Lactobacillus*
	Ruminococcaceae	*Faecalibacterium*
		Ruminiclostridium
		Ruminococcus
	Streptococcaceae	*Streptococcus*
	Veillonellaceae	*Veillonella*
Proteobacteria	*Enterobacteriaceae*	*Escherichia*

1.2. Archaeome

Archaea are prokaryotic microorganisms morphologically very similar to bacteria, but with significant biochemical and molecular differences in cell structure, which allowed them to be distinguished into a separate kingdom (domain). They play an important role in the human (and animal) gastrointestinal tract, being in metabolic symbiosis with bacteria and contributing to the host's digestive processes. The aggregate of archaea in the human or animal gastrointestinal tract is called an archaeome, the archaeome consists of a large number of taxa (Fig. 5) [9].

The figure shows that the human gastrointestinal microbiome contains representatives of most taxa (order level) of archaea. The majority of the representatives belong to methanogens (orders *Methanobacteriales* and *Methanomassilicoccales*), i.e. those that produce methane as a metabolite by assimilating hydrogen and carbon dioxide produced by bacteria. In addition to the gut, methanogens are also found in the oral cavity.

It is known that archaea in the normal microbiota of the human body live not only in the intestines, but also in the nasal cavity and on skin [10], as well as in the oral cavity [11]..

At the same time, there is evidence of the potential role of archaea in reducing the risk of certain human diseases (in particular, atherosclerosis), and thus the possibility of their use as probiotics [12].

1.3. Mycobiome

Fungi are eukaryotic heterotrophic decomposing organisms. They occupy an important place in the microbiomes of humans and animals: they are present in the microbiota of the gastric rumen in ruminants and on the skin of humans and animals, as well as in the intestines. Both yeast and mycelial fungi are present on human skin (including the ear canals and genitalia) and in the intestines (Table 2) [13].

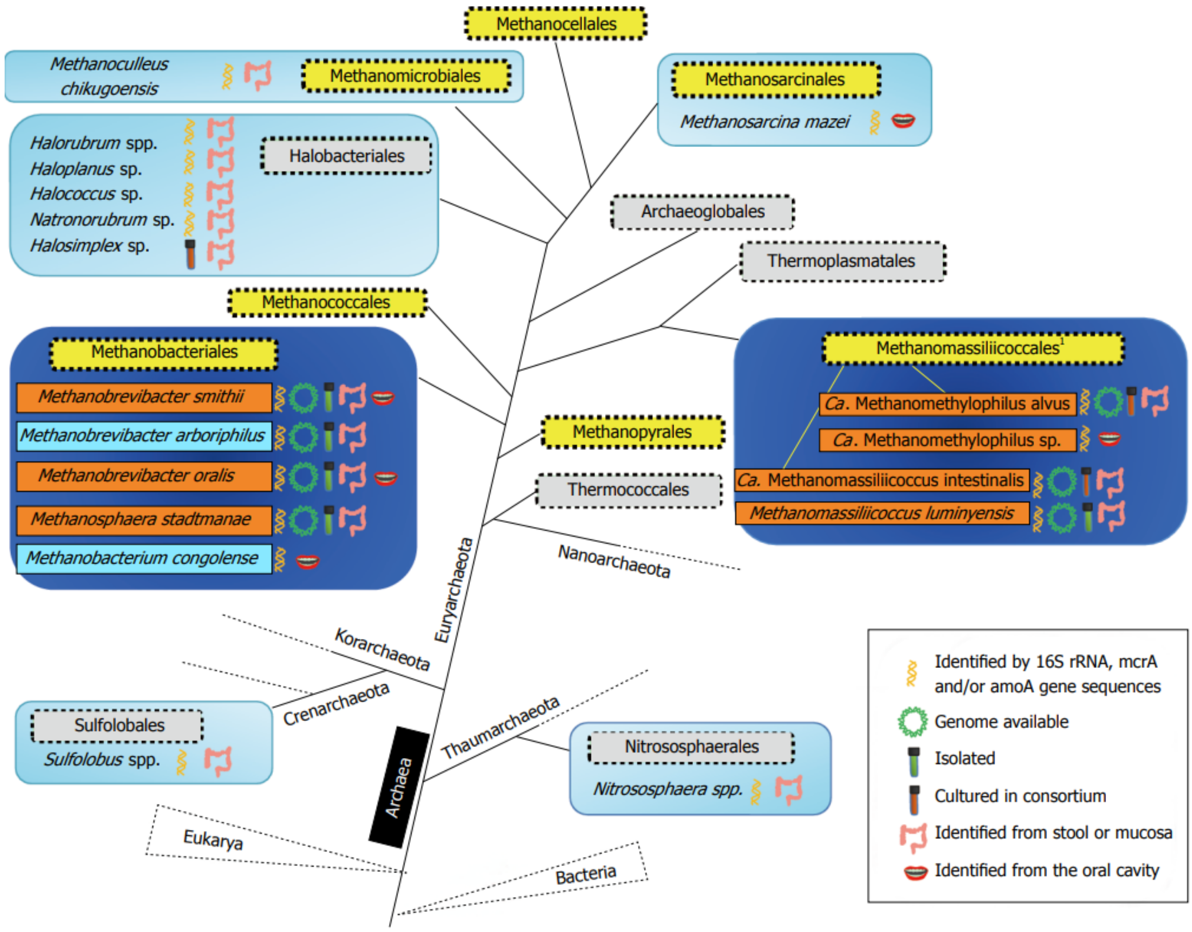


Fig. 5. Archaeal taxa present in the human gastrointestinal tract archaeome according to [9]

Table 2: Fungal taxa found in the human gastrointestinal tract according to [13]

Genera	Species
Candida	*C. albicans*
	C. tropicalis
	C. parapsilosis
	C. glabrata
	C. krusei
	C. lusitaniae
Saccharomyces	*S. cerevisiae*
Penicillium	*P. commune*
Aspergillus	*A. versicolor*
Cryptococcus	
Malassezia	*M. globosa*
	M. restricta
	M. pachydermatis
Cladosporium	*C. herbarum*
Galactomyces	*G. geotrichum*
Debaryomyces	*D. hansenii*
Trichosporon	

Among the fungi in this table, the genera *Cryptococcus*, *Malassezia*, and *Trichosporon* belong to the division *Basidiomycota*, and the rest of the genera belong to *Ascomycota*. In other words, only higher fungi are present in the intestinal mycobiome, while representatives of other orders are also present in the mycobiomes of the stomach and intestines of animals (see Part 1). However, there is also evidence of fungi of the genus *Mucor* (*Zygomycota*) in human intestinal contents, and in vegetarians – representatives of *Agaricus* (mushrooms) and epiphytic-phytopathogenic genera *Alternaria* and *Epicoccum* [14].

Studies show that fungi in the gut microbiome are in constant connection with bacteria and demonstrate a correlation in numbers [15, 16], and at the same time play an important role: they modulate immune activity and the development of inflammatory processes, promoting the activation of certain groups of T-helper cells [17].

1.4. Virome

A virome is a collection of viruses that inhabits a particular biome (in which their hosts live). Viruses of both eukaryotes and prokaryotes (bacteriophages) are found in the normal microbiomes of animal and human organisms. At the same time, bacteriophages make up about 90% of the virome, and viruses of eukaryotes – less than 10% (Table 3) [18].

As can be seen from the table, the diversity of viruses in the human gut is quite large and variable throughout life: it differs significantly between infants and adults. The number of viruses associated with diseases increases significantly with age.

Table 3 – Composition of intestinal viromes in infants under 1 year of age and adults according to [18]

Viral group	**Genome**	**Viral taxa in infants under 1 year of age**	**Viral taxa in adults**
Bacterio-phages	Double-stranded DNA	*Myoviridae, Podoviridae, Siphoviridae, Corticoviridae, Tectiviridae, Amandaviridae, Sisseviridae, Picoviridae, Skunaviridae, β-crassviridae, Jeppeviridae, Alberteviridae, Hannahviridae, Flandersviridae, Evaviridae*	*Myoviridae, Podoviridae, Siphoviridae,* crAss-phages
	Single-stranded DNA	*Inoviridae, Microviridae, Gokushoviridae, Alpaviridae, Inesviridae, Almaviridae, Noraviridae, Circoviridae*	*Inoviridae, Microviridae*
Viruses of eukaryotes	Double-stranded DNA	*Adenoviridae**, *Polyomaviridae**	*Adenoviridae**, *Herpesviridae**, *Iridoviridae**, *Marseilleviridae, Mimiviridae**, *Papillomaviridae**, *Polyomaviridae**, *Poxviridae**
	Single-stranded DNA	*Anelloviridae**, *Circoviridae, Geminiviridae, Nanoviridae, Parvoviridae**, *Genomoviridae**	*Anelloviridae**, *Circoviridae, Parvoviridae**
	Double-stranded RNA	*Picobirnaviridae**, *Chrysoviridae, Reoviridae**	*Picobirnaviridae**, *Reoviridae**
	Single-stranded RNA	*Caliciviridae**, *Astroviridae**, *Virgaviridae, Picornaviridae**, *Alphaflexiviridae, Tombusviridae*	*Caliciviridae**, *Astroviridae**, *Virgaviridae, Picornaviridae**, *Retroviridae**, *Togaviridae**, *Alphaflexiviridae, Bromoviridae, Luteoviridae*
Viruses of archaea		*Lipothrixviridae*	

* Viruses associated with human diseases

Studies show that the infant's intestinal virome depends on the feeding method: during breastfeeding, some viruses (bacteriophages and others) enter the baby's organism with milk [19]. Bacteriophages modulate the activity of the bacterial part of the microbiome by lysing (killing) some cells and changing the properties of others through the appearance of prophages in them, and this balance is influenced by various factors, such as diet, the state of health of the intestines and the whole organism, taking certain medications, etc. It has been shown that bacteriophages of human intestinal virome can not only cause antibiotic resistance in bacteria by introducing new genetic material, but also modify their genome by interfering with CRISPR sequences [21].

2. The role of the gastrointestinal microbiota in shaping human health

The role of the intestinal microbiota in human life is well researched and shows a huge contribution to the majority of physiological processes and the formation of most mechanisms that underlie the vital activity of the human body.

Fig. 6 shows a diagram of the impact of human intestinal microecology on the health according to [22].

The figure demonstrates the incredible complexity and sophistication of the molecular mechanisms of influence of the gut bacteria on a number of physiological processes in the human body: fat deposition (obesity), atherosclerosis, liver disorder, type II diabetes (due to impaired insulin sensitivity), inflammation, and neuroregulatory shifts. Bacteria in the microbiota produce (either on their own or when processing human food substances) certain substances that directly or indirectly cause certain cellular reactions. The list of these substances is huge: short-chain fatty acids (acetic, butyric, propionic, caproic, valeric), indole derivatives (indole, indoxyl sulfate, indolylpropionic acid), bile acid metabolites (deoxycholic and lithocholic acids), choline metabolites (choline, trimethylaminoxide, betaine), phenolic derivatives (equol, urolithins, enterolactone, enterodiol, phenylnaringenin, etc.), vitamins (thiamine, riboflavin, niacin, pyridoxine, pantothenic and folic acids, biotin, cobalamin, menaquinone), polyamines (putrescine, spermidine, spermine) [23].

A positive effect of supporting microbiota with probiotics on the course of a number of diseases was shown, the diseases include non-intestinal disorders: diarrhea of various etiologies, necrotizing enterocolitis, respiratory infections, urinary system infections, asthma, eczema, fungal infections, Crohn's disease, cystic fibrosis, type II diabetes, depressive mental disorders, and chronic periodontitis [24].

2.1. Gut-brain axis

The neuroregulatory influence of the microbiota has attracted the attention of scientists in the 21st century and has been studied to some extent. These studies have shown the existence of what is known as gut-brain axis, i.e., the pathway of physiological influence of the gut microbiota on human brain activity. A diagram of this axis is shown in Fig. 7 [25].

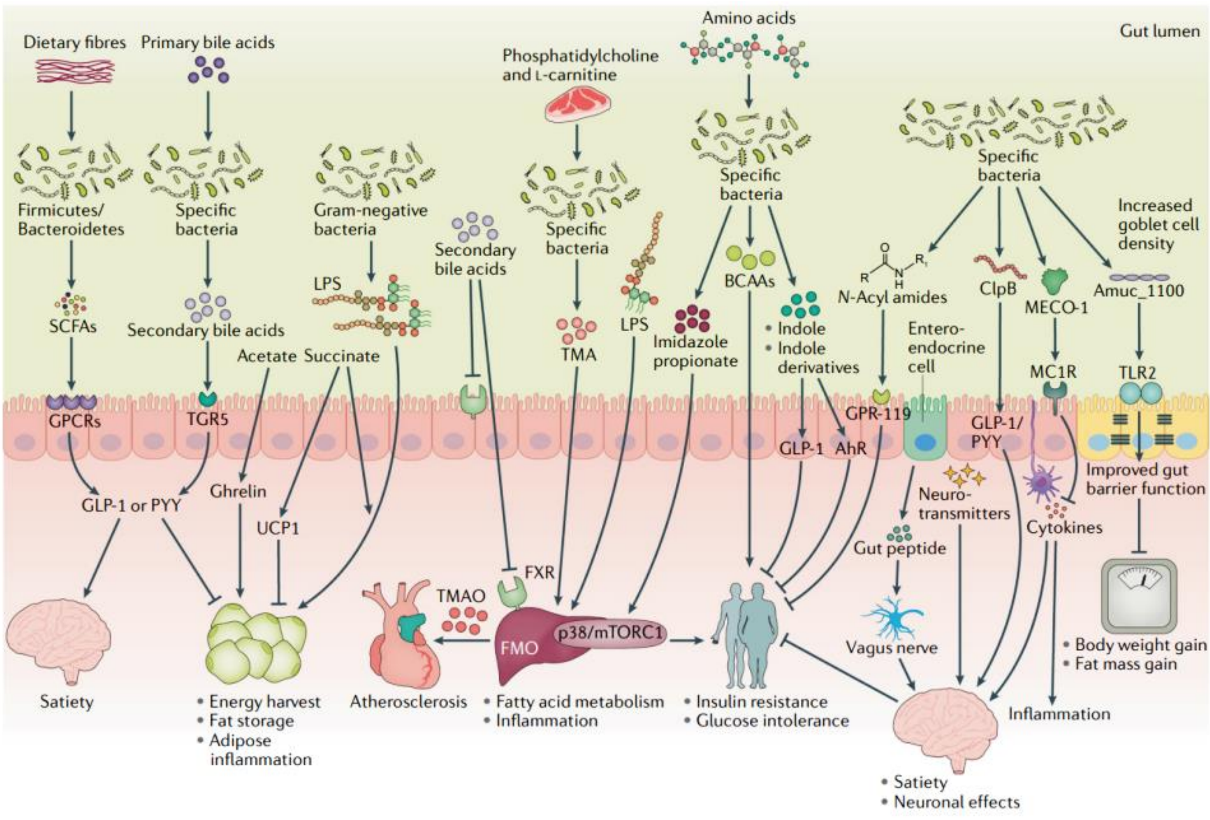
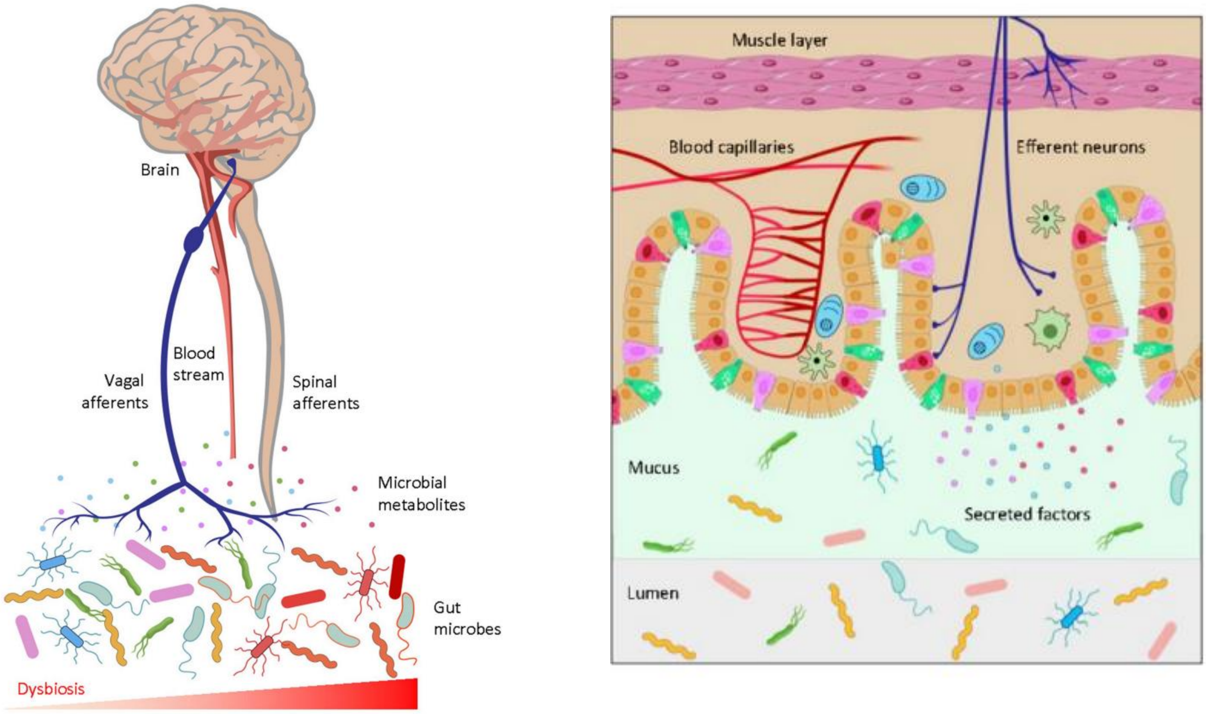


Fig. 6. Influence of gut microbiota on human physiological processes and its consequences [22]



a) *b)*

a – afferent influence of the microbiota, b – efferent action of the nervous system

Fig. 7. The gut-brain axis in humans according to the paper [25]

As can be seen from the figure, the gut-brain axis represents the reciprocal influence between the gastrointestinal microbiota and the central nervous system. The microbiota produces metabolites and biologically active substances that trigger impulses that reach the brain in various ways: directly via the vagus nerve, through the bloodstream, or through the spinal canal. In turn, the central nervous system sends impulses that activate secretory cells in the intestinal mucosa (goblet cells, Paneth cells, and others), which produce mucus with biologically active substances (e.g., lysozyme and defensins).

Medical studies have shown the influence of the gut microbiota (through the gut-brain axis) on the risk of stroke and its consequences and complications [26], as well as the development and course of Alzheimer's disease [27]. In addition, certain correlations have been observed between the gut microbiome and the course of other diseases: autism spectrum disorders, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, Huntington's disease, and depressive disorders [28].

3. Food microbiota and its impact on the human gastrointestinal microbiota

The microbiota of food products is not uniform and depends entirely on the composition of the product, its manufacturing and storage conditions. Below (Table 4) is a summary of the most important groups of microorganisms in food products according to [29].

The microorganisms listed in the table include both saprophytic microbiota (most bacteria, fungi, yeasts), which can cause food spoilage, and pathogenic forms (protozoa, viruses, some bacteria), which cause food poisoning and infectious diseases. Fungi can also cause poisoning due to the release of mycotoxins, which are their toxic metabolites.

Another publication [30] pays great attention to the microbiota of meat and meat products (Table 5).

These data indicate a huge diversity of food microbiota, even within the same food group. The publication of the International Commission on Microbiological Specifications for Foods (ICMSF) [31] defines the most important (by the degree of risk to human health) microbiological indicators (Table 6) and methods and ways to control them.

3.1. Impact of food microbiota on human intestinal microbiota

This issue has not been studied to date. According to the authors of [32], only the effect of probiotic preparations used to correct intestinal microbiome disorders is well covered, and the role of the general non-pathogenic microbiota of foods is unknown. It can be assumed that this impact will be strongest on the health of infants and preschool children due to an unstable, underdeveloped microbiome, and in the elderly due to the decline of their own normal microbiome.

Table 4 – The most important genera of microorganisms in food according to [29]

Group	Genera
Bacteria	
Gram-negative aerobic or microaerophilic motile curved rods	*Campylobacter, Arcobacter, Helicobacter*
Gram-negative aerobic straight rods and cocci	*Pseudomonas, Xanthomonas, Acetobacter, Gluconobacter, Acinetobacter, Moraxella, Alteromonas, Flavobacterium, Alcaligenes, Brucella, Psychrobacter*
Gram-negative facultatively anaerobic rods	*Citrobacter, Cronobacter, Escherichia, Enterobacter, Edwardsiella, Erwinia, Hafnia, Klebsiella, Morganella, Proteus, Salmonella, Shigella, Serratia, Yersinia, Vibrio, Aeromonas, Plesiomonas*
Rickettsia	*Coxiella*
Gram-positive cocci	*Micrococcus, Staphylococcus, Streptococcus, Enterococcus, Lactococcus, Leuconostoc, Pediococcus*
Gram-positive spore-forming rods	*Bacillus, Sporolactobacillus, Clostridium*
Gram-positive non-spore-forming rods	*Lactobacillus, Carnobacterium, Brochothrix, Listeria, Corynebacterium, Brevibacterium, Propionibacterium, Bifidobacterium*
Mycelial fungi	
Ascomycota	*Aspergillus, Penicillium, Alternaria, Fusarium, Geotrichum*
Zygomycota	*Mucor, Rhizopus*
Yeasts	
Ascomycota	*Saccharomyces, Pichia, Torulopsis, Candida, Zygosaccharomyces*
Basidiomycota	*Rhodotorula*
Viruses	
Pathogenic	Hepatitis A, noroviruses, polioviruses, adenoviruses, ECHO viruses, coxsackieviruses, rotaviruses, sapoviruses, hepatitis E
Bacteriophages	Numerous, affecting many bacterial genera
Protozoa	
Intestinal parasites	*Giardia, Cryptosporidium, Cyclospora, Cystoisospora, Toxoplasma*

Table 5 – The most common microorganisms on meat, poultry, meat products, fish and seafood in total according to [30]

Groups of microorganisms		
Bacteria	Mycelial fungi	Yeasts
Achromobacter, Acinetobacter, Aeromonas, Alcaligenes, Alteromonas, Arthrobacter, Bacillus, Brochothrix, Buttiauxella, Campylobacter, Carnobacterium, Chromobacterium, Citrobacter, Clostridium, Corynebacterium, Cytophaga, Enterobacter, Enterococcus, Escherichia, Flavobacterium, Hafnia, Halobacterium, Janthinobacterium, Klebsiella, Kluyvera, Kocuria, Kurthia, Lactobacillus, Lactococcus, Leuconostoc, Listeria, Microbacterium, Micrococcus, Moraxella, Morganella, Paenibacillus, Pantoea, Photobacterium, Proteus, Providencia, Pseudomonas, Rahnella, Serratia, Shewanella, Staphylococcus, Streptococcus, Vibrio, Weissella, Yersinia	*Alternaria, Acremonium, Aspergillus, Aureobasidium, Botrytis, Cladosporium, Chrysosporium, Fusarium, Geotrichum, Monascus, Monilia, Mucor, Neurospora, Penicillium, Rhizopus, Scopulariopsis, Sporotrichum, Thamnidium*	*Candida, Cryptococcus, Debaryomyces, Hansenula, Pichia, Rhodotorula, Saccharomyces, Torulopsis, Trichosporon*

Table 6 – The most important microbiological indicators in different types of food products according to ICMSF [31]

Product category	Indicators
Meat and meat products	*Salmonella*, toxigenic *E. coli*, *Campylobacter jejuni/coli, Yersinia enterocolitica, Staphylococcus aureus, Clostridium perfringens, Clostridium botulinum, Listeria monocytogenes, Bacillus cereus, Shigella*
Poultry and poultry products	*Salmonella*, thermophilic *Campylobacter*, *Clostridium perfringens, Listeria monocytogenes, Staphylococcus aureus, Clostridium botulinum*
Fish and seafood	*Clostridium botulinum* (some cases), *Vibrio*, coliforms, viruses, *Staphylococcus aureus, Listeria monocytogenes*
Vegetables and vegetable products	*Listeria monocytogenes, Clostridium botulinum, Salmonella, E. coli, Bacillus cereus, Staphylococcus aureus,* molds
Fruit and fruit products	*E. coli, Salmonella*, molds, *Listeria monocytogenes* (fresh pre-cuts), *Clostridium botulinum* (canned fruit)

Product category	Indicators
Dry spices and dry concentrates	Depends on how the product will be used
Grain and grain products	Molds, *Salmonella*, *Staphylococcus aureus* (pasta)
Nuts, oilseeds and legumes	Molds, *Salmonella*
Cocoa, chocolate and confectionery	Depends on the type of product, usually *Salmonella* and staphylococci
Oil and fat products	*Salmonella*, *E. coli*, *Listeria monocytogenes*, *Staphylococcus aureus*, *C. botulinum* (sometimes)
Sugar, syrups and honey	*Clostridium botulinum* (honey)
Soft drinks, fruit juices, fruit concentrates and preserves	*Salmonella*, *E. coli*, molds
Water	*Campylobacter jejuni*, *E. coli* O157 and similar strains, *Salmonella* spp., *Shigella* spp., *Vibrio cholerae*, *Yersinia enterocolitica*, viruses
Eggs and egg products	*Salmonella*, *Listeria monocytogenes*
Milk and dairy products	Various, depending on the region of production and type of product, mostly *C. botulinum*, *Bacillus* spp., *Salmonella*, *Staphylococcus*, *Listeria monocytogenes*
Fermented beverages	Molds

Conclusion

The human intestinal microbiome is a highly complex multicomponent system that provides vital functions of the host organism. Food products also contain a well-developed microbiome, although it is unstable and non-uniform. This microbiome may contain pathogenic species of microorganisms for humans, but the impact of the non-pathogenic microbiota of foods (except for probiotic preparations) has not been studied and should be the subject of future research.

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МІКРОБІОМИ ШЛУНКОВО-КИШКОВОГО ТРАКТУ ЛЮДИНИ, СВІЙСЬКИХ ТВАРИН, ХАРЧОВИХ ПРОДУКТІВ І КОМБІКОРМІВ: ЗВ'ЯЗОК ТА ВПЛИВ. ЧАСТИНА 2

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Анотація. Дослідження мікробіому шлунково-кишкового тракту людини, що почалися достатньо давно, сьогодні проводяться новітніми сучасними методами та створюють новий погляд та уявлення. Мікробіом кишковика людини містить мільярди мікробних клітин в 1 г кишкового вмісту. Серед цих мікроорганізмів присутні представники всіх надцарств: прокаріоти (царства бактерій та археїв), еукаріоти (гриби) та віруси. Таксономічний склад при цьому містить сотні видів бактерій, десятки видів археїв та грибів, десятки родин вірусів. Вони постійно перебувають у тісному зв'язку та взаємодії як один з одним, так і з клітинами та тканинами хазяїна. Є дані про потенційну роль археїв-метаногенів у розвитку певних хвороб, а гриби та бактерії є корисними симбіонтами, що чинять значний вплив на здоров'я хазяїна. Віруси представлені здебільшого бактеріофагами, що модулюють популяції бактерій. Вплив на здоров'я людини реалізується через складні молекулярні механізми: мікроорганізми виділяють біологічно активні метаболіти, що модулюють клітинно-тканинну біохімічну активність і через неї – роботу імунної системи та інших органів тіла людини, включаючи центральну нервову систему. В свою чергу, організм людини відповідає з боку нервової та імунної систем та місцевих тканин кишковика, що утворюють певні речовини, які модифікують діяльність мікроорганізмів. Це призводить до утворення кишково-мозкової вісі, що складається з аферентного (до мозку) та еферентного (від мозку) шляхів. Є дані про кореляції між складом мікробіоти та розвитком низки кишкових та некишкових хвороб, в тому числі нейродегенеративних та поведінкових. Мікробіота кишковика людини непостійна протягом життя людини, і суттєво відрізняється за віком (від немовляти до похилого віку) за частками різних таксонів. Водночас харчові продукти містять сотні видів мікроорганізмів, тобто різних бактерій та грибів (дріжджів та міцеліальних). Ця мікробіота продуктів може чинити вплив на мікробіоту кишковика, особливо у ранньому (немовлята, діти дошкільного віку) та похилому віці. Однак це питання не досліджено і має вивчатися в майбутньому.

Ключові слова: мікробіом, шлунково-кишковий тракт, мікроекологія, кишково-мозкова вісь, імунна відповідь, харчові продукти.