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## MICROBIOMES OF HUMAN, LIVESTOCK ANIMAL GASTROINTESTINAL TRACTS AND OF FOOD PRODUCTS AND COMPOUND FEEDS: CONNECTIONS AND IMPACTS. PART 1

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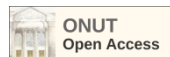
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### Introduction. Formulation of the problem

To date, a lot of knowledge has been accumulated on the physiological mechanisms of assimilation of food substances by the gastrointestinal tract (GIT) of animals of different species, both herbivores and carnivores. These mechanisms are directly determined by the gut structure and the diet of animals. These mechanisms are different for monogastric omnivores (pigs), monogastric herbivores (horses), and ruminants (cattle), and the physiology of digestion in mammals is markedly different from that in birds.

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**Abstract.** The physiological mechanisms of food digestion in humans and feed digestion in animals are determined by the structure of the gastrointestinal tract (GIT) and diet. Accordingly, humans are omnivores, while domestic animals are divided into ruminants, monogastric herbivores, and monogastric omnivores, and birds are divided into herbivores (geese, ducks) and omnivores (chickens, turkeys, etc.). The digestion and assimilation of food and feed depends not only on own mechanisms but also on the GIT microbiome. The location of the most important part of this microbiome and its composition depend on the species: in ruminants, it is the rumen microbiome, in horses – the cecum (it is a counterpart of the rumen), in humans and pigs – the intestine, in birds – the crop, gizzard and cecum. These microbiomes are in constant close connection with the host organism, and this connection is realized through numerous molecular mechanisms of interaction between bacterial cells and host cells and tissues. GIT microorganisms not only help to assimilate food (feed) by partially digesting it, but also secrete biologically active substances that have protective, stimulating and other beneficial effects for the host. In adult hosts, this GIT microbiota is well developed and stable, while in children and young animals it can be much more mobile and vulnerable. Food and feed contain many components that are a favorable medium for the development of microorganisms. Raw materials and components of animal origin are the most contaminated, while vegetable raw materials and components, as well as premixes, contain significantly fewer microorganisms. Among the microorganisms colonizing raw materials, food and feeds, coliforms, salmonellae and molds may be present. In young animals, the feed microbiota ingested into the GIT, even without taking into account obligate or opportunistic pathogens, can cause shifts or changes in the digestive microenvironment towards deterioration, which will have a corresponding impact on the efficiency of feed absorption and, through it, on the efficiency of feeding and animal productivity.

**Keywords:** microbiome, gastrointestinal tract, microecology, compound feeds, food products, immune response.

In livestock, these mechanisms have not changed since the animals were domesticated, but new studies have been conducted on them to identify the impact of various factors on the absorption of various types of feed, including compound feed. Among these factors, the state of the microbiota of the most important GIT parts of the (stomach or certain parts of the intestine) has proven to be vital. Based on studies of the impact of gastrointestinal microbiomes on feed conversion, probiotic preparations have been developed and implemented to maintain animal health and productivity [1].

However, there is another aspect of this issue: the impact of the microbial population of industrially produced feed on the GIT microecology of animals, and thus on their productivity. No deep studies have been conducted on this issue.

The study of the gastrointestinal microbiota of farm animals in terms of its role in maintaining animal health and productivity began long ago, when the general effect of normal gastrointestinal microbiota on human and warm-blooded vertebrate health was described. Not only has the impact of normal microbiota on productivity (in the case of monogastric animals, weight gain, in the case of poultry – egg production and quality) been recognized, but probiotic agents have been developed that are added to feed to improve the microbiota, which in turn improves digestion and nutrient assimilation and, consequently, productivity [2].

The problem of this work was to outline the potential interconnections between the animal gut microbiota and the compound feed microbiota in terms of potential improvement of feeding efficiency and productivity of livestock farming.

The **purpose** of this work was to estimate the relations between the animal gut microbiome and the compound feed microbiomes, primarily for young animals.

The **objectives** of this work included the following:

1) to review the literature about the animal gut microbiomes, the impact and role of gut microbiota in the animal's life and about the compound feed microbiota;

2) to outline potential impacts of compound feed microbiota on the young animal's health for further research.

## Analysis of recent research and publications

### 1. Gut Microbiota of Livestock

Today, the microbiomes of human, animal, and other organisms are studied not by culturing microbes, but by two modern methods:

1) Metagenomic studies, i.e. isolation of total DNA or 16S rRNA from the environment with its subsequent examination for the presence of fragments and sequences characteristic of certain taxa of microorganisms (from phylum to species). This method is used today to study the gastrointestinal microbiota of farm animals, including in dynamics. The results are expressed not via the number of microbial cells or colony-forming units (CFU) per unit mass or volume of the substrate, but via the number of copies of the corresponding DNA or 16S rRNA and the relative abundance of genetical markers [3,4].

2) Metaproteomic studies: the study of the entire set of proteins obtained from the microbiota of a particular substrate, with the isolation of those characteristic of certain taxa of microorganisms. This method

complements metagenomics with data on the protein composition of the microbiota [5,6].

The review given below contains data obtained by these two methods.

#### 1.1 Gut Microbiota of Ruminants

The gastrointestinal tract of ruminants is characterized by a complex structure due to the presence of a complex, multi-chambered stomach.

The first and largest compartment of the stomach (up to 80% of the total volume), the *rumen*, is known to contain an abundant multicomponent microbiome, including, in addition to bacteria, archaea, protozoa, and fungi. This compartment is fermentative, i.e., it provides microbiological fermentation and partial decomposition of the food mass.

The second section, the *reticulum*, is much smaller and serves to separate coarse particles that are then sent back to the rumen. Rumen microorganisms enter the reticulum along with the food mass.

The third compartment, the *omasum*, absorbs water, minerals, and fatty acids. The omasum also contains rumen microorganisms that get there along with the food mass.

The fourth and last compartment, the *abomasum*, is glandular and performs the function of enzymatic digestion of food by the animal's own enzymes. Its acidic secretion and enzymes kill most of the microbiota that comes with food from the rumen.

##### Microbiota of rumen

*Bacteria*. It is known from the literature [7] that most of the rumen microbiota in ruminants is represented by bacteria, the number of which is about 1000 CFU/ml of rumen contents. Table 1 shows the main categories of rumen bacteria.

**Table 1 – Main categories of rumen bacteria [7]**

Bacterial category	Examples of species
Cellulolytic	<i>Fibrobacter succinogens</i> , <i>Ruminococcus flavefaciens</i> , <i>Ruminococcus albus</i> , <i>Clostridium longisporum</i> , <i>Eubacterium cellulosolvans</i> , <i>Clostridium cellobioparum</i>
Hemicellulolytic	<i>Eubacterium xylanophilum</i> , <i>Eubacterium uniformis</i> , <i>Prevotella ruminicola</i>
Lipolytic	<i>Anaerovibrio lipolytica</i>
Pectolytic	<i>Treponema saccharophilum</i> , <i>Lachnospira multiparus</i>
Proteolytic	<i>Prevotella</i> sp., <i>Ruminobacter amylophilus</i> , <i>Clostridium bifermentans</i>
Amylolytic	<i>Prevotella ruminicola</i> , <i>Streptococcus bovis</i> , <i>Ruminobacter amylophilus</i>
Saccharolytic	<i>Succinivibrio</i> sp., <i>Lactobacillus</i> sp., <i>Bifidobacterium ruminantium</i>
Tanninolytic	<i>Streptococcus caprinus</i> , <i>Eubacterium oxidoreducens</i>
Ureolytic	<i>Megasphaera elsdenii</i>

*Archaea* make up up to 3.6% of the rumen microbiota, almost all of them belong to methanogens (species that produce methane as a metabolite), with *Methanobrevibacter* being the dominant genus (up to 26.5%). They utilize carbon dioxide, hydrogen, and some organic compounds produced by bacteria, releasing methane in the process.

*Protozoa* make up a large part of the rumen microbiome – up to 50% of the biomass. They are represented mainly by ciliates and flagellates, with ciliates being predominant. Their main function is the digestion of coarse fibrous substances, and they are in metabolic symbiosis with bacteria and archaea.

*Fungi* account for up to 20% of the rumen microbiota. They are represented mainly by asexual forms of the *Chytridiomycetes* (up to 8% of the rumen microbiota), which are involved in the breakdown of coarse fibrous substances. Rumen fungi, like protozoa, are in metabolic symbiosis with bacteria.

Some *bacteriophages* also reside permanently in the rumen, lysing bacterial and archaeal cells. During this lysis, many bacterial proteins are released to become material for other processes [8].

**Table 2 – Non-bacterial rumen microbiota [7,8]**

Group of organisms	Examples
Archaea	<i>Methanobacterium</i> , <i>Methanobrevibacter</i> , <i>Methanomicrobium</i> , <i>Methanosarcina</i> , <i>Methanoculleus</i>
Protozoa	<i>Entodinium</i> , <i>Epidinium</i> , <i>Isotricha</i> , <i>Dasytricha</i> , <i>Diplodinium</i> , <i>Oligoisotricha</i> , <i>Polyplastron</i> , <i>Eremoplastron</i>
Bacteriophages	Methanobacterial phages $\psi$ M1, M10, M100, M2 etc.
Fungi	<i>Piromyces</i> , <i>Anaeromyces</i> , <i>Caecomyces</i> , <i>Cyllamyces</i> , <i>Neocallimastix</i> , <i>Orpinomyces</i>

It should be noted that the intestines of ruminants also have a certain microbiota, but it is not as important for digestion as the rumen microbiota, which contains all the main processes of microbial digestion.

### 1.2 Gut Microbiota of Pigs

Pigs (*Sus domesticus*) are monogastric animals, that is, they have a simple stomach, not divided anatomically or physiologically into compartments typical of ruminants. Their stomach is glandular, not fermentative, so there is little microbiota in it, and the main amount of the latter is concentrated in the colon [9,10] (Fig. 1).

The figure shows that the stomach is the poorest part of the piglet's gastrointestinal tract, while the cecum and large intestine are the richest in microbiota. This is due to the most favorable conditions for microbiota development in this part of the gastrointestinal tract.

The amount of microbiota in CFU/g of intestinal contents is estimated at  $10^8$  or more, and its taxonomic composition is variable throughout the life of

the animal and depending on other factors that will be discussed below.

During metagenomic analysis, the taxonomic composition of the microbiota is determined by taxon rank: from highest to lowest, i.e. from phylum to species. Therefore, the literature data contain information in this form.

Fig. 2 shows the data of the study [11] with the exact separation by periods before and after piglets are weaned from their mothers. These data reveal the details of the taxonomic composition of the microbiome: the most numerous taxa are *Prevotella* and *Firmicutes*. It can also be seen that within the *Firmicutes* phylum, the family *Ruminococcaceae* and the genus *Lactobacillus* predominate.

### 1.3 Gut Microbiota of Horses

Horses are monogastric animals, i.e. they have a simple one-compartment stomach. However, microbiological digestion of food takes place in the large intestine and the cecum, which are of considerable size: the horse's cecum can have a volume of up to 90 liters, and the total length of the intestine reaches 26 meters. It is the cecum and the proximal parts of the large intestine that contain the fermenting microbiota in horses [12].

The microbiota of the horse cecum consists of a huge number of bacteria (up to  $10^9$  CFU/g) from more than 100 genera, as well as a large number of archaea, protozoa, and fungi [13].

Table 3 shows the main genera of bacteria in the equine cecum that are most important for maintaining the health of the animal.

The table shows that the microbiome of the horse cecum is very similar to the rumen microbiome and, accordingly, performs similar functions in the digestion of food mass (in particular, the decomposition of coarse fibers).

### 1.4 Gut Microbiota of Chickens

The gastrointestinal microbiota of birds differs from that of mammals due to differences in gastrointestinal structure and feeding physiology. In birds, the most microbiota-rich parts of the GI tract are the crop, gizzard, small intestine, and ceca. Available publications contain a lot of data on the gastrointestinal microbiota of chickens. Fig. 3 shows the composition of the microbiota of the chicken cecum according to the study [14].

It shows that anaerobic cocci (ruminococci) predominate in the cecum, but they also live in the gastrointestinal tract of other animals. The predominance of anaerobic microorganisms is also noticeable, it is due to the appropriate medium conditions in this part of the gastrointestinal tract.

Studies of chickens from different regions have shown that their intestinal microbiota is not the same and depends on the region (Fig. 4) [15], which is explained by differences in feeding, the feeds used, housing conditions, and climatic conditions of the region.

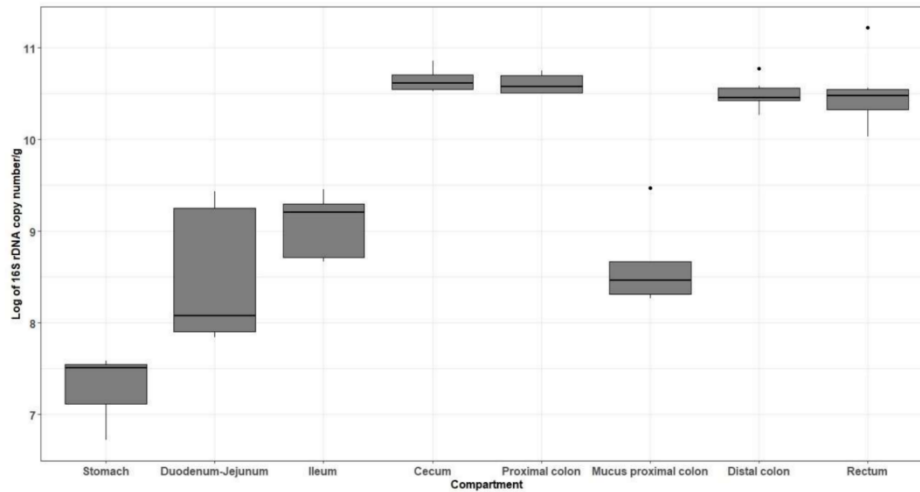
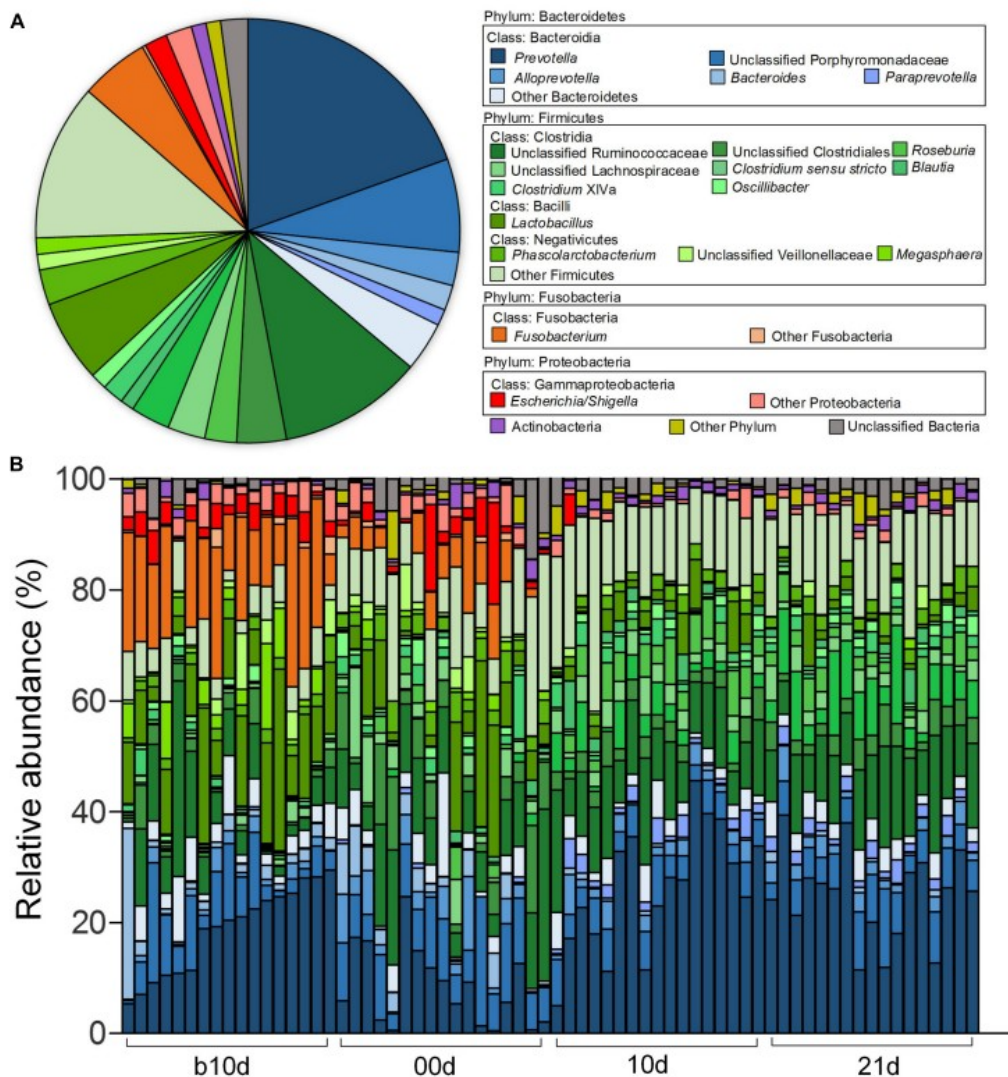


Fig. 1. The amount of microbiota in different parts of the piglet GIT according to [9]



A – main genera, B – relative abundance of these main genera;  
 b10d – 10 days before weaning, 00d – the day of weaning, 10d – 10 days after weaning,  
 21d – 21 days after weaning

Fig. 2. Composition and dynamics of piglet gut microbiome at the genus level according to [11]

Table 3 – Composition of the fermentative microbiota of the horse gut according to [13]

Kingdom	Family	Genus, description
Bacteria	<i>Ruminococcaceae</i>	<i>Ruminococcus</i>
	<i>Fibrobacteraceae</i>	<i>Fibrobacter</i>
	<i>Streptococcaceae</i>	<i>Streptococcus</i>
	<i>Lactobacillaceae</i>	<i>Lactobacillus</i>
	<i>Acidaminococcaceae</i>	<i>Mitsuokella, Phascolarctobacterium</i>
	<i>Veillonellaceae</i>	<i>Veillonella</i>
	<i>Lachnospiraceae</i>	<i>Butyrivibrio, Blautia</i>
	<i>Clostridiaceae</i>	<i>Clostridium</i>
	<i>Eubacteriaceae</i>	<i>Eubacterium</i>
	<i>Prevotellaceae</i>	<i>Prevotella</i>
	<i>Succinivibrionaceae</i>	<i>Ruminobacter</i>
Fungi	<i>Enterococcaceae</i>	<i>Enterococcus</i>
	<i>Neocallimastigaceae</i>	<i>Piromyces</i>
Protozoa	Ciliates, flagellates	
Archaea	Methanogens	
Bacteriophages	Parasites of bacteria	

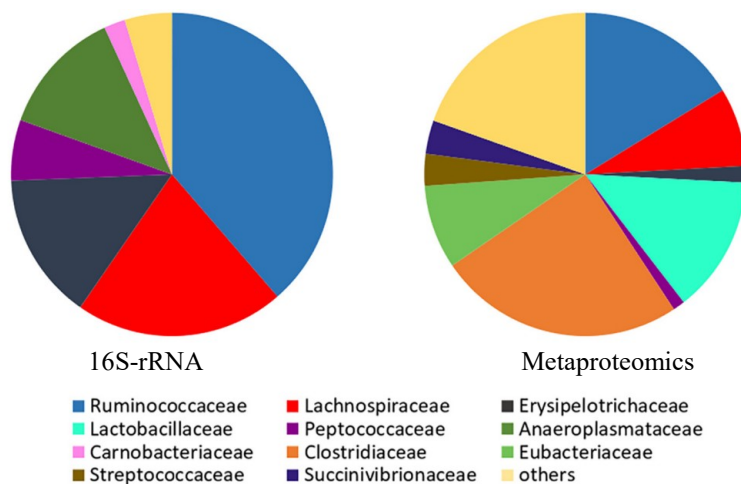
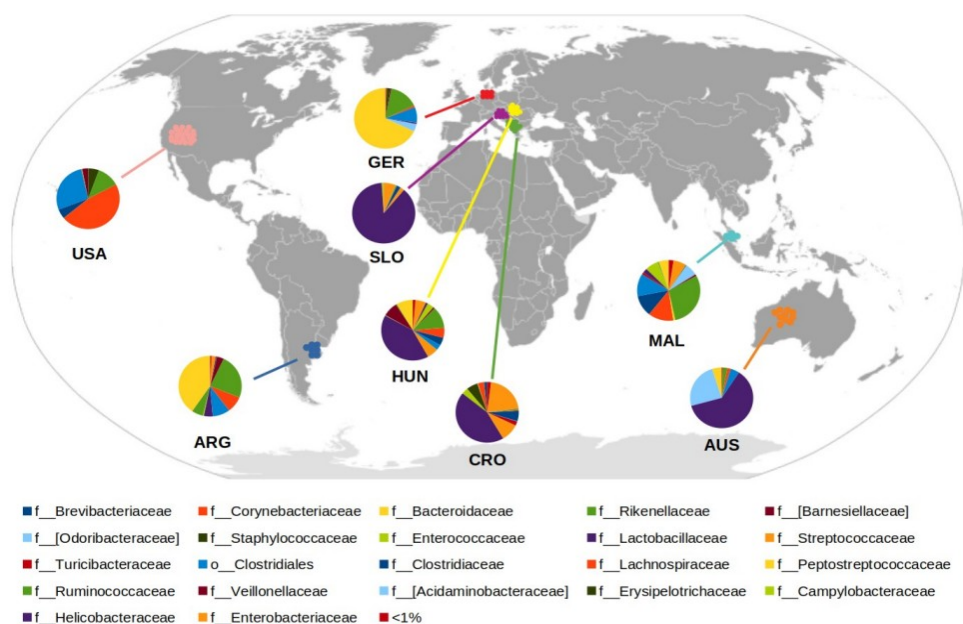


Fig. 3. Composition of the microbiota of the chicken cecum according to [14]



GER – Germany, USA – United States of America, SLO – Slovenia, HUN – Hungary, CRO – Croatia, MAL – Malaysia, ARG – Argentina, AUS – Australia

Fig. 4. Geographical differences in the gastrointestinal microbiota of chickens at the family level [15]

### 1.5 Gut Microbiota of Ducks and Geese

The digestive tracts of geese and ducks have a structure similar to that of other birds, although ducks are naturally omnivorous birds (they feed on both animal and plant foods in nature and need protein feedstuffs), while geese naturally have an almost exclusively vegetable diet with a large proportion of coarse fiber, and need less protein feed. As a result, geese have large ceca that help digest food.

Figures 5 and 6 show the metagenomic data on the composition of the gastrointestinal microbiome of

geese at the level of phyla and families according to [16].

These figures show that there is a marked difference in the gastrointestinal microbiomes of geese in different types of housing – caged and floor. In caged housing, there were significantly higher levels of *Firmicutes* (gram-positive spore-forming and non-spore-forming bacteria), *Proteobacteria* (which include enterobacteria) and *Actinobacteria*, which include actinomycetes and bifidobacteria.

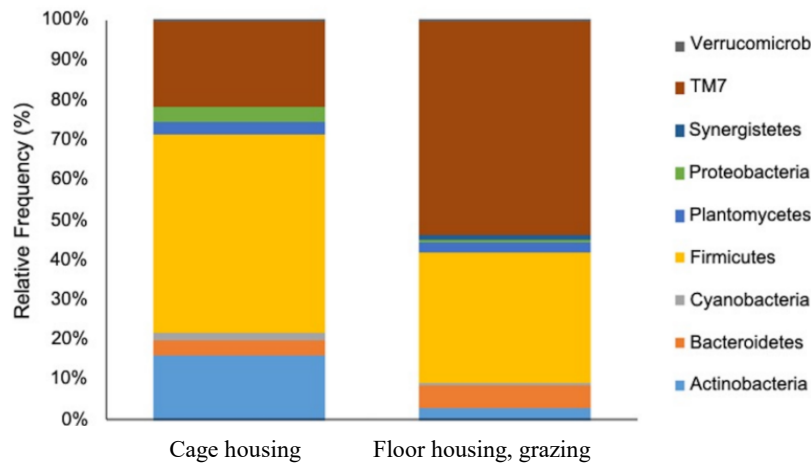


Fig. 5. Composition of goose gut microbiome according to [16], phylum level

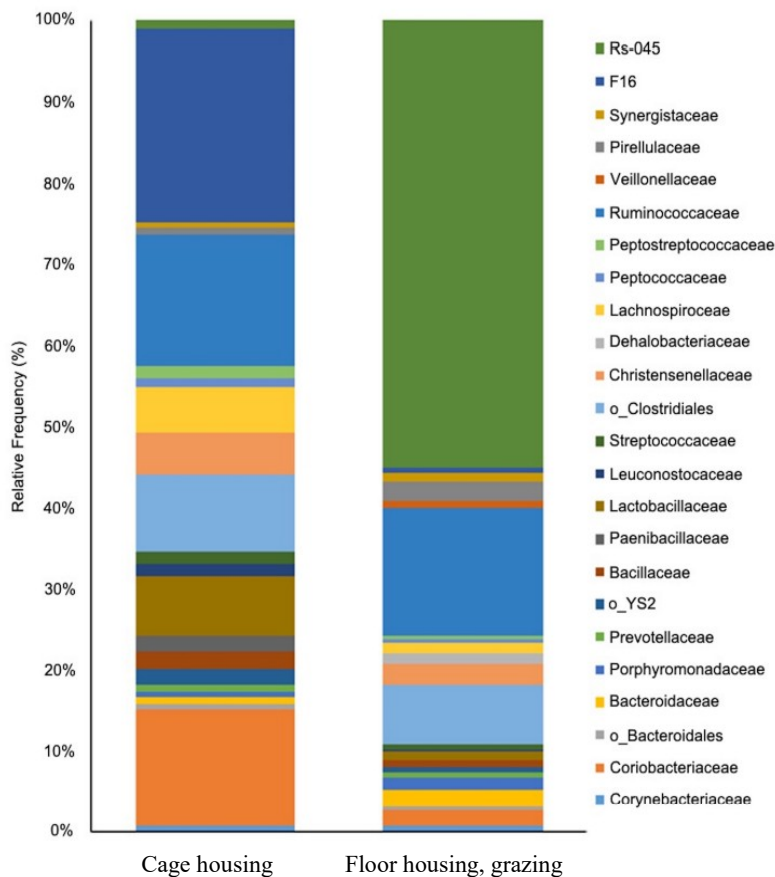


Fig. 6. Composition of goose gut microbiome according to [16], family level

## 2 The role of the gastrointestinal microbiota in animal vital activity

Today, there is a wealth of evidence to support the vital importance of maintaining a normal microbiota in the digestive tract of livestock. Without such support, animals lose their health and therefore their productivity.

The microbiota of the animal gastrointestinal tract, just like in humans, is in close contact with the host body at the tissue and cellular levels, which affects the condition of these tissues and cells, and therefore affects the digestion and health of animals.

Figure 7 summarizes the development of the intestinal mucosa in mice with a developed microbiota and in sterile animals [17].

The figure shows that in the absence of a normal microbiota, all components of the mucous membrane were disrupted: the formation of epithelium, local immune tissues and cells, vascularization, and innervation. These processes are due to complex molecular interactions of the microbiota with the host organism at the cellular level [18]. It is clear that under such influence, the importance of the animal's microbiota for maintaining its growth and productivity is enormous. In particular, the stimulation of T and B-lymphocyte proliferation and antibody production is

of great importance for local immunity, which protects against pathogens.

In ruminants, the rumen microbiota breaks down the coarse fiber substances of the feed (cellulose, hemicellulose, lignin, pectins), allowing the animal to digest them [19]. These processes are carried out simultaneously by bacteria, fungi, and protozoa, which are in close symbiosis with each other.

The following important functions of the microbiota are known for piglets [20]:

- transformation of substances that cannot be degraded by the animal's own enzymes, with the release of substances useful for the animal, such as long-chain fatty acids; these acids serve as a source of energy for epithelial cells;
- limiting the access of pathogenic microorganisms to the intestinal epithelium through the formation of a protective layer;
- stimulation of the immune system, which enhances protection against pathogenic microorganisms;
- increase in feed conversion and, consequently, feed efficiency; this is well observed during weaning of piglets from mothers with transfer to starter feed, which is often accompanied by severe diarrhea due to microbiota disorders.

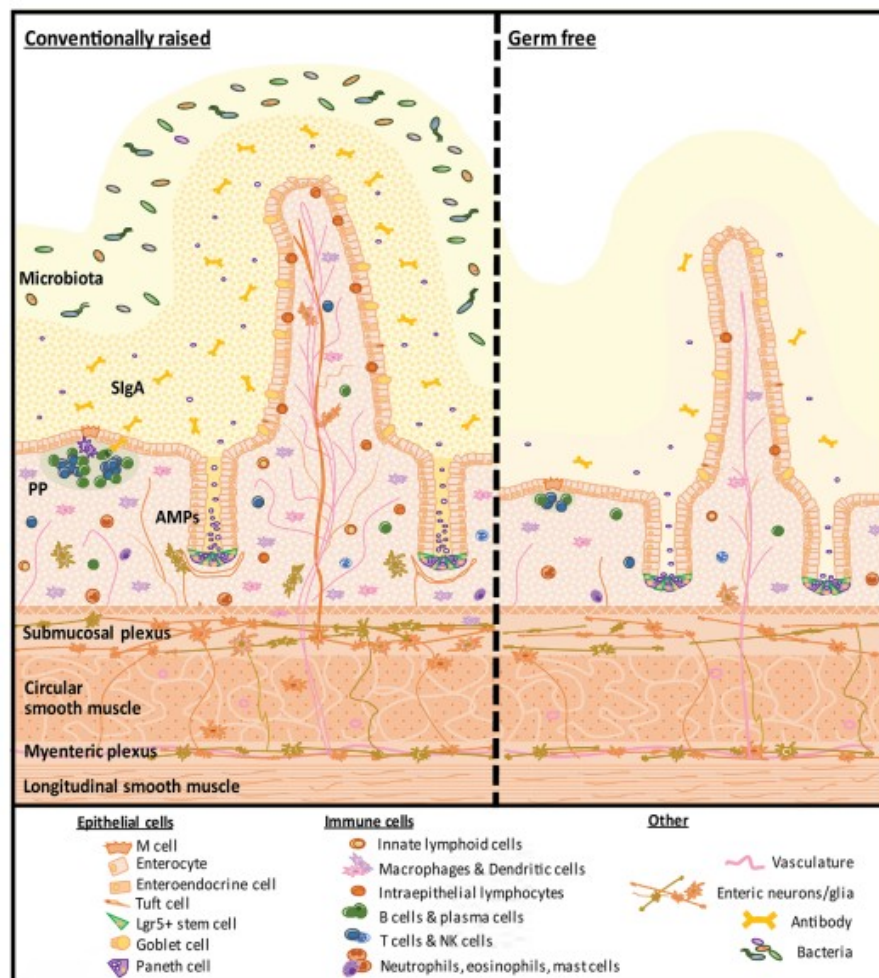


Fig. 7. Development of intestinal mucovilli in normal and germ-free mice [17]

For chickens, there is also evidence of the role of the microbiota [14]: just like in the case of piglets, it stimulates the development of intestinal cells, prevents the penetration of pathogens, and stimulates the immune system, accordingly affecting feed conversion and animal productivity.

In all warm-blooded animals, the most important in this context is the lactic acid microbiota and bifidobacteria, because these have the greatest positive effect on the host, as described above.

### 2.1 Mechanisms of interaction between microbiota and host organism

In many microbiomes, symbiotic relationships arise between microorganisms, in which participants depend on each other to some extent, for example, using each other's metabolites as a source of energy or carbon. However, due to the density of microbiomes with insufficient resources in most substrates, competition for these resources arises. The most essential resources for microorganisms are nutrients and space.

There are two ways of competition between microorganisms [21] (Fig. 8):

- indirect, or passive: outperforming a competitor in the struggle for resources without directly harming it;
- direct or active: damage to competitor cells.

The first pathway is realized via increasing the uptake of substances or the release of exoenzymes for their utilization, as well as the utilization of the competitor's exometabolites. In addition, rapid colonization of the substrate before the competitor is possible, which is also achieved by various substances that accelerate growth or movement or enhance attachment to the surface. For the same purpose, biofilms – microbial aggregates on surfaces – are formed. In this case, the competitor will have to somehow destroy the aggregate to take its place.

Active competition is realized through the release of antimicrobial substances – antibiotics, which can have either a very narrow (strain or species level) or a very broad (family, order, class, non-taxonomic group level) spectrum of action. In addition, there is the T6 secretion system (T6SS), through which microorganisms introduce various substances, mostly proteins, into each other's cells, while simultaneously taking away part of the genetic material from the opponent [22].

Since the number of microorganisms in the normal microbiota usually far exceeds the number of pathogens coming from the outside, such competition helps protect the host from pathogens.

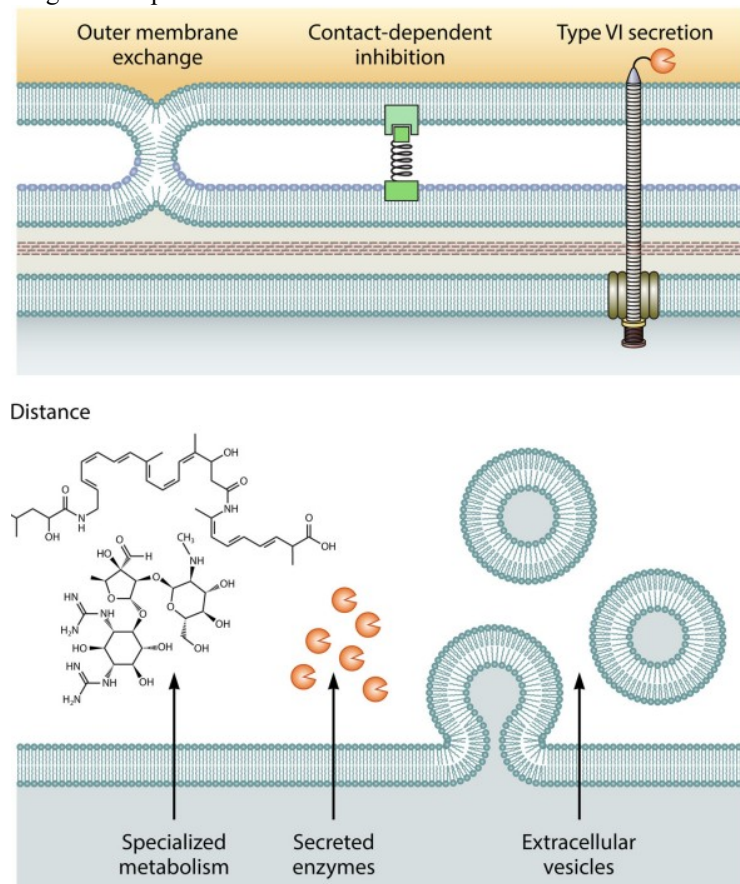


Fig. 8. Ways of competition between microorganisms according to [21]

## 2.2 The burden on the immune system and the role of microbiota in it

The body's immune response is a complex multi-stage process by which the body resists external foreign agents – antigens. This process involves the activation of many types of immune cells, their interaction and the synthesis of humoral factors (antibodies, complement, interferons, etc.) [23]. All these processes require certain energy expenditures, which the body receives from digested and assimilated food (feed). This energy absorbed from the feed is called metabolized energy [24]. Therefore, in terms of animal growth performance, the expenditure of metabolized energy on the immune response instead of productivity is an undesirable factor, especially for young animals, for which such an impact must be particularly harmful.

This implies the need to limit the expenditure of metabolic energy on the immune system of the animal, so that more of it remains for productivity.

Respirometry is the only generally accepted method for determining the energy expenditure of a living organism and the intensity of its energy metabolism. This method is based on measuring oxygen consumption and carbon dioxide release during respiration of the tested organism, indicating the intensity of energy metabolism in the body. And knowing the amount of energy (J) per unit volume of oxygen (ml), it is possible to calculate the energy metabolism of the animal. Literature data contain quite diverse results obtained on various laboratory and specially captured animals [25].

Thus, according to Martin and Scheuerlein [26], in house sparrows, stimulation of the cellular immune response significantly (by 28.8% of resting energy) increased the level of metabolic activity, which means corresponding energy expenditure. In blue [27] and great tits [28], the primary humoral response increased metabolic activity by 7.8%, and the secondary response in blue tits [27] by 12.7%. In laboratory mice [29], the primary humoral response increased energy metabolism by 27.4%. For the leaf-nosed bat, there are data on an increase of only 2% [30], and for the fish-eating myotis – by 185% [31].

It has been shown in piglets that after stimulation of the immune system with a vaccine, there was a decrease in weight gain with a decrease in feed intake and an increase in feed conversion [32], which is explained by increased metabolic activity aimed at the immune response to the vaccine.

These data show that activation of the immune response may require mobilization of a significant portion of the energy consumed by the body from food (feed), so it is worth limiting the immune burden for young animals so that energy is not spent on resisting microorganisms.

Thus, maintaining the normal microbiota of an animal, including by limiting the immune burden, has a significant impact on its productivity, and attention

should be paid to this aspect in animal farming. To date, probiotics have been developed to be added to feed for such support, but preventing problems (diseases) is known to be much more effective than solving them (treatment, recovery).

In view of the above, the development of methods for the in-flow disinfection of feed in production can significantly improve the state of the livestock industry.

## 3. Sanitary Condition of Raw Materials and Finished Feed

The microbiota of raw materials and finished feeds is not the same in different types of raw materials and feeds of different composition. In addition, the microbial contamination of loose and pelleted feeds also differs.

Table 4 shows the data compiled from several works [33,34,35,36,37,38] on the levels of microbial contamination of feed and feed raw materials at plants of earlier technological generations.

**Table 4 – Levels of contamination of raw materials and feed according to Sokolov et al. [33-38]**

Substrate	Indicator value
<b>Bacteria, content level, CFU/g</b>	
Grain raw materials	270,0 thousand
Bran	371,0 thousand
Non-grain vegetable raw materials	965,0 thousand
Animal raw material	2,8 million
Premixes	757,0 thousand
Finished feeds	1,99 million
<b>Fungi, content level, CFU/g</b>	
Grain raw materials	44,2 thousand
Bran	5,0 thousand
Non-grain vegetable raw materials	7,0 thousand
Animal raw material	6,3 thousand
Premixes	1,2 thousand
Finished feeds	27,3 thousand
<b>Coliforms, % of samples with presence</b>	
Grain raw materials	35,0
Non-grain and animal raw materials	57,4
Finished feeds	70,8
<b>Other sanitary indicators</b>	
Staphylococci (total), % of samples with presence	49,3
<i>Staphylococcus aureus</i> , % of samples with presence	16,0
Toxigenic fungi, % of all recovered cultures	29,4
Salmonellae, % of samples with presence	22,8
Enteropathogenic <i>E. coli</i> , % of samples with presence	5,1

These data indicate a rather high level of microbial contamination of feed raw materials and finished feed, which can be a very unfavorable factor in terms of animal productivity due to the negative impact on their health.

This picture is complemented by a modern study of the microbiota of poultry feed [39], conducted using

modern methods. Fig. 9 shows the indices of the numbers of microbial species in poultry feed.

The figure shows that blood meal and meat and bone meal, two types of high-protein animal feedstuffs, were the richest in microbiota. Sorghum and corn were the poorest in terms of species diversity, although this does not mean that the number of microbial cells is low. At the same time, the microbiota in finished feeds was not very rich in species composition.

The taxonomic composition of the microbiota of poultry feed according to this study is shown in Table 5.

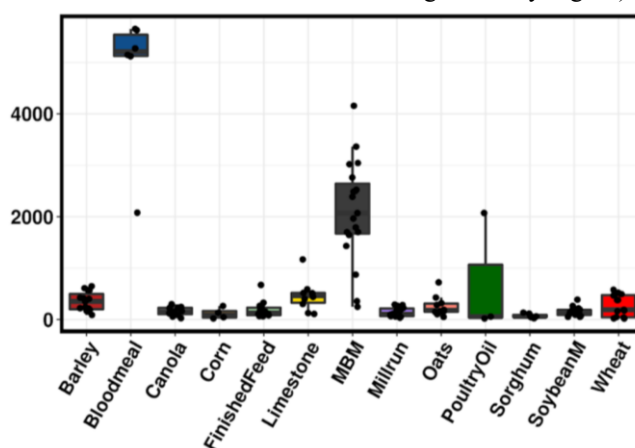
**Table 5 – Taxonomic composition of the microbiota of poultry feed according to [39]**

Bacterial phylum	% of markers
<i>Actinobacteria</i>	47,6
<i>Proteobacteria</i>	38,9
<i>Firmicutes</i>	11
<i>Bacteroidetes</i>	2,5

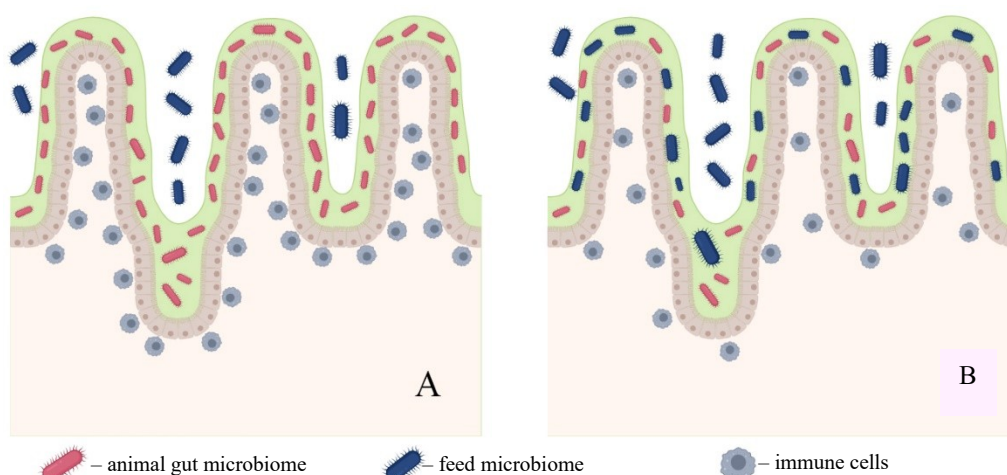
A total of 50 genera were identified: *Arthrobacter*, *Acinetobacter*, *Aerococcus*, *Bacillus*, *Bifidobacterium*, *Blautia*, *Brachy bacterium*, *Brevibacterium*, *Clostridium*, *Comamonas*, *Coprococcus*, *Corynebacterium*, *Dietzia*, *Enterobacter*, *Enterococcus*, *Facklamia*, *Frigoribacterium*, *Jeotgalicoccus*, *Lactobacillus*, *Lactococcus*, *Leuconostoc*, *Microbacterium*, *Oscillospira*, *Paenibacillus*, *Proteus*, *Pseudochrobacterium*, *Ruminococcus*, *Sphingobacterium*, *Sporosarcina*, *Staphylococcus*, *Streptococcus*, *Trichococcus*, *Turicibacter*, *Wautersiella* and 15 unrecognized genera.

The above shows that the microbiota of feed can significantly affect the state of the animal's gastrointestinal tract, interfering with its normal microbiome and causing an immune response. The overall outline is shown in Fig. 10.

The figure shows that the gut mucous membrane of an adult animal is much better protected than that of young animals (the number of microorganisms in its own normal microbiome and protective immune cells is significantly higher).



**Fig. 9. Indices of numbers of bacterial species in compound feeds for poultry and their raw materials by metagenomic data according to results of research [39]**



**Fig. 10. Scheme of interference of the feed microbiota with the gastrointestinal microbiome**  
 A – adult animal, B – young animals at early growth stage (pre-starter or starter feed)

Therefore, it is young animals that will suffer significantly from high levels of contamination of feed with microorganisms: the latter can not only disrupt the unformed microbiome and threaten to cause diseases, but also cause an undesirable immune response.

### Conclusion

These data indicate a considerable diversity and quantity of the gastrointestinal microbiota of animals, which is in a complex and sophisticated interaction

with the host. The equilibrium of this interaction can be disturbed if a large number of microorganisms are ingested with food (feed). Feed raw materials and finished feed contain a huge number and variety of microorganisms that, when ingested, cause an immune response. All of this can have a corresponding impact on the microenvironmental state of the gastrointestinal tract of young animals, and thus on their health, and eventually on their productivity.

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## МІКРОБІОМИ ШЛУНКОВО-КИШКОВОГО ТРАКТУ ЛЮДИНИ Й СВІЙСЬКИХ ТВАРИН ТА ХАРЧОВИХ ПРОДУКТІВ І КОМБІКОРМІВ: ЗВ'ЯЗОК ТА ВПЛИВ. ЧАСТИНА 1

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**Анотація.** Фізіологічні механізми засвоєння їжі у людей та корму у тварин визначаються будовою шлунково-кишкового тракту (ШКТ) та раціоном. Відповідно, людина є всеїдною, а свійські тварини поділяються на жуйних, моногастричних травоядних та моногастричних всеїдних, птахи – на рослиноїдних (гуси, качки) та всеїдних (кури, індики та ін.). Травлення та засвоєння їжі й корму залежить не лише від власних механізмів, а але й від мікробіому ШКТ. Розташування найважливішої частини цього мікробіому та його склад залежить від біологічного виду: у жуйних найбільше значення має мікробіом рубця шлунка, у коней – мікробіом сліпої кишки (аналог рубця), у людини та свиней – кишкового, у птахів – вола, м'язового шлунка та сліпих кишок. Ці мікробіоми знаходяться в постійному тісному зв'язку з організмом хазяїна, цей зв'язок реалізується через цілу низку молекулярних механізмів взаємодії бактеріальних клітин між собою та з клітинами і тканинами хазяїна. Мікроорганізми ШКТ не лише допомагають засвоїти їжу (корм) шляхом їхнього часткового перетравлення, але й виділяють біологічно активні речовини, які мають захисну, стимулюючу та іншу корисну для хазяїна дію. У дорослих хазяїв ця мікроекологія ШКТ достатньо розвинута і стійка, а у дітей та молодняка може бути значно рухливішою та вразливішою. Харчові продукти та комбікорми містять багато компонентів, які є сприятливим середовищем для розвитку мікроорганізмів. Найбільш забрудненими є сировина та компоненти тваринного походження, рослинні сировина й компоненти та премікси містять помітно меншу кількість мікроорганізмів. Серед мікроорганізмів, що колонізують сировину, харчові продукти та комбікорми, можуть бути присутні кишкові палички, сальмонели та плісеневі гриби. У молодняка тварин при потрапленні в шлунково-кишковий тракт мікробіота продукту або корму, навіть без урахування патогенних або умовно-патогенних мікроорганізмів, може спричинити зсуви або зміни у мікроекології травлення в бік погіршення, що відповідним чином відобразиться на ефективності засвоєння корму і відтак через неї – на ефективності годівлі та продуктивності тварини.

**Ключові слова:** мікробіом, шлунково-кишковий тракт, мікроекологія, комбікорми, харчові продукти, імунна відповідь.