

DESCRIPTION FOR THE GENERAL PUBLIC

Microbiome is defined as the whole ecological environment composed of commensal, symbiotic, and pathogenic microorganisms that rise to the rank of a master, previously underestimated organ. Intestinal microbiome seems to decide on many aspects of life, including the use and processing of food, or health. In the first days after hatching, the digestive system of birds is the most intensively developing organ, stimulated to do so by bacteria colonizing it (microbionts). Domination of microorganisms that are capable of rapid proliferation and adherence to the mucosa occurs due to fast movement of the intestinal contents. In a double ceca occurring in birds, the flow of contents is slowed down, which creates good conditions for settlement of many microorganisms and formation of proper intestinal microbiome. The relationship between the intestinal microbiome and the host is formed evolutionarily in the nature of symbiosis, or even mutualism.

The majority of digestible sugars derived from a diet is digested and absorbed in the initial sections of the intestine, where the number of bacteria is small. Only indigestible polysaccharides and unabsorbed residues are substrates for microorganisms colonizing the end fragments of the intestines. Polysaccharides, oligosaccharides, or disaccharides are decomposed by microorganisms into simple sugars which are then subjected to bacterial fermentation to form short-chain fatty acids, mostly acetic, propionic and butyric acids. These again become the host's source of energy and carbon, and absorbed by the intestinal epithelial cells and incorporated into many metabolic cycles of the host. Short-chain fatty acids not only reduce the pH of the intestinal environment, thus controlling the composition of microbionts, but also in an undissociated form diffuse into the cells of many bacteria, and lower their pH, thus affecting the metabolism of these bacteria. Additionally, butyric acid is an energy source for intestinal epithelial cells, it enhances their growth and proliferation, regulates intestinal blood flow and mucus production. It also modulates the local immune responses.

Bacterial fermentation takes place practically in every segment of the intestinal tract, beginning with the crop, and ending in ceca, but the most intensive one occurs in the latter. The hydrogen, which is produced during the fermentation inhibits this process, and thus has a negative impact on the host. Hydrogen consumers are therefore desirable. In the majority of intestinal microbiomes methanogenic microorganisms are the prominent hydrogen consumers. Data on their prevalence in ceca of chickens are variable and some authors, in an indeed small percentage, confirm the presence of methanogenic archaea in the amount of 2 per cent, while others do not detect them. Another group of microorganisms that can potentially utilize hydrogen are sulfate-reducing bacteria, mainly of the genus *Desulfovibrio*, but their presence is questioned by some researchers. Another process, in which the hydrogen can be used, is the synthesis of acetic acid by the reduction of CO₂ and the formation of acetyl-CoA. This type of reaction is carried out by bacteria from Ruminococcaceae and Lachnospiraceae families. Enzymes necessary for hydrogen utilization are also found in bacteria of the genera *Megamonas*, *Wolinella*, *Helicobacter* and *Campylobacter*. Unfortunately, the latter, especially *Campylobacter jejuni*, represent an important etiological agent of food poisoning in humans. For this reason, various attempts are made, the purpose of which is to eliminate the pathogen from the gastrointestinal tract of chickens, and increase the safety of poultry products. Authors of many scientific publications have demonstrated the ability to reduce intestinal colonization of these pathogens by administering probiotic *Lactobacillus* strains. However, since *C. jejuni* is a hydrogen consumer, it is assumed that after its elimination, in order to provide the continuity of fermentation, other consumers of hydrogen will multiply, and take over the role of *C. jejuni*. To test this hypothesis an experiment will be performed, in which the animals will be inoculated with a certain *Lactobacillus* strain, an antagonist of *C. jejuni*. An assumed effect of the research will be the reduction or elimination of *Campylobacter*, and the potential increase of other microorganisms involved in the hydrogen sink.