

A group of microorganisms that inhabit the digestive tract of chickens is called microbiota. Bacteria are the main component of this collection. The intestinal microbiota is considered to be a specific ecosystem that has a significant impact on the functioning of the entire organism. Local microflora plays a key role in the prevention and treatment of microbial infections and is often referred to as the "forgotten organ".

Not only the host influences the composition of its microbiota, but also the microbiota positively influences the host, e.g. its metabolism, nutrition, development and modulation of immunity and response to infection. Microbiota is now recognized as a regulator of many host physiological functions and goes far beyond its role in digestion. During illness, the composition of the microbiota changes significantly. Such imbalance is called dysbiosis or dysbacteriosis. It is associated with many diseases. Virus-induced dysbacteriosis can promote the multiplication and transmission of viruses in organisms.

Infectious bronchitis virus (IBV), the coronavirus causing infectious bronchitis (IB), leads to one of the largest economic losses in chicken industry in Poland and in the world. Along with highly pathogenic avian influenza (HPAI) and Newcastle disease (ND), IB is the most economically important respiratory viral disease affecting the world poultry industry.

There are many IBV genotypes/variants that differ genetically from each other and infect various tissues/organs/systems. However, it should be remembered that the main route of entry of all IB viruses is through the respiratory system. Therefore, the project planned to assess both intestinal and respiratory microbiota after infection of chickens with IB virus. With lung small intestine tissue samples and the use of the modern molecular biology methods, we plan to conduct detailed microbiota studies. We will evaluate the qualitative and quantitative composition of bacteria in virus infected chickens compared to healthy ones. In the experiment we will use two strains representing different genotypes.

In the project, we also planned forced changes in the quantitative composition and qualitative structure of the microbiota. We want to achieve this through the use of broad-spectrum antibiotic therapy. We assume that such changes will affect the chickens' response to the infection, which in turn will alter the course of the disease. Antibiotic therapy is intended to serve as a model for dysbiosis (disturbances in the structure and composition of the microbiota) in early life. In practice, it can occur as a result of poor nutrition, antibiotic therapy or infection.

Such an in-depth analysis will be possible thanks to the use of the most modern methods of molecular biology. To determine the type and number of bacteria, we will use next-generation sequencing (NGS) in the "metagenomic" approach, i.e. the analysis of DNA isolated directly from microorganisms present in a given environment. Until recently, this was done primarily by cell culture methods. These unfortunately have many limitations: they cannot be used for bacteria that do not grow in cell culture, and they are also selective for bacteria that easily proliferate in cultures. Ultimately, the obtained nucleotide sequences will be subjected to bioinformatic analysis, which will allow each bacterium to be classified into a given taxonomic group. The planned studies will also allow us to demonstrate the differences in virus-microbiota and microbiota-virus interactions caused by two different genotypes.

The results of the project will allow to understand the role of the microbiome in the course of IB virus infection. They will give an answer if and how the modification of the microbiome (depletion) influences the course of infection already at its first stages. Besides the cognitive aspects, the obtained results will help to understand the molecular mechanisms involved in the host microbiota-virus interactions. This may allow, in the future, to further improve vaccines or implement preventive measures to modify the gastrointestinal microbiota with probiotics or targeted antibiotic therapy, which in turn could alleviate the symptoms of the disease or prevent its occurrence. Knowledge of the mechanisms involved in IBV pathogenesis is still scarce, and understanding them is also crucial in the context of the current SARS-CoV-2 pandemic.