

Growing consumer awareness of the impact of animal welfare on the quality of meat and eggs and increased social sensitivity to animals' suffering create the need to implement modern breeding systems based on animal welfare. This requires additional financial outlays, but reduces the mortality of animals in the herd, and increases the quality of meat and eggs, and food safety. Intensive production and errors or negligence in breeding lead to a decrease in herd immunity, and susceptibility to diseases, including bacterial ones. It consequently leads to the use of antibiotics and the spread of antibiotic resistance. This may result in bacterial contamination and antibiotic residues in food.

Industrial poultry farming covers laying (laying hens) and meat (broilers) production. Farmers use feed and feed additives dedicated to the age of the birds and the intended breeding effects. However, backyard farming is based mainly on traditional feeding and the availability of natural resources (insects, plants). The breeding strategy has a large impact on animal welfare, which is reflected in the intestinal microbiota, including bacteria, fungi, viruses, and parasites. The bacterial intestinal microbiota of poultry supports digestion, synthesizes vitamins, inhibits the growth of pathogens, and stimulates the immune system, and its composition depends mainly on dietary and environmental factors. The fungal microbiota (mycobiota) of poultry is much less known. Some studies showed a similar role to the bacterial microbiota and suggest the possibility of modulating the intestinal mycobiota to prevent diseases and improve production parameters. Parasites inhabiting the intestines of chickens can cause up to 10-20% of production losses, and viral infections can course from asymptomatic to severe and economically devastating

However, the level of well-being is difficult to assess reliably. In the case of poultry, it includes counting feet with pathological changes on the soles, daily mortality rate, and assessment of the farm's physical parameters based on designated standards and ranges. These methods are simple and cheap, but they do not provide information about stress factors, an unbalanced diet, or the risk of infection. The use of modern molecular biology methods to study the intestinal microbiome in connection with animal welfare could fill this diagnostic gap. The research aims to understand the composition of the poultry intestinal microbiome in various breeding systems. It will be used to assess the possibility of using modern molecular biology methods to assess the level of welfare of these animals and the risk of infection in the herd.

As part of the project, the intestinal microbiome of broiler, laying hens and backyard chickens will be examined. High-throughput sequencing is a modern method that makes it possible to obtain the genetic composition of organisms inhabiting a given environment, in this case, the intestines of poultry. All organisms present in the intestine can be sequenced using the shotgun metagenomics approach, which generates high costs and a huge amount of data. Additionally sequencing only regions important from the researcher's point of view (targeted metagenomics) is applied, which significantly reduces the costs of analyses. In the project targeted sequencing will be used for all tested samples and will enable the determination of bacterial (analysis of the 16S rRNA gene) and fungal (analysis of the ITS region) composition in the samples. In turn, shotgun metagenomics will be used on pooled samples of every group to identify parasites or viruses, whose full composition cannot be determined using targeted methods. The activity of enzymes produced by bacteria will also be examined. The composition and diversity of the intestinal microbiome of chickens from different breeding systems will be analyzed in terms of the presence and abundance of bacteria and fungi that may be beneficial to health, or predispose chickens to the development or cause diseases. Particular attention will be paid to the relationship between the bacterial and fungal microbiome. The research will be used to examine the possibilities of implementing the genomics methods to assess poultry welfare and infection risk.