

DESCRIPTION FOR GENERAL PUBLIC

The bacterial community that lives in the gastrointestinal tract, known as the gut microbiome, is important for proper functioning of the whole organism. The microbiome helps provide proper nutrition for the host, thus improving its health. Recent studies show that the composition of this community in the gut of human may affect the proliferation of tumor cells in their bodies, cause mental diseases or even autism. This findings suggest that the microbiota of the gastrointestinal tract has a bigger impact on the functioning of the whole organism than has been expected before. Compared to the microbiome studies of the gastrointestinal tract of mammals that are conducted for years, microbiome of fish still remains a black box. One of the most important issue in aquaculture is to determine the relationship between bacterial community of gastrointestinal tract both of wild and farmed fish and their health. Thus, the comparative analysis of microbiota of the gastrointestinal tracts will be a interesting task in research. This project will focus on tench (*Tinca tinca*), that is a common species in natural body of water and it is considered as important species in aquaculture.

In fish microbiomes, some bacteria that accumulate polyhydroxyalkanoates (PHAs) could be present. PHAs are a large group of polymers, which have similar properties to synthetic polymers and are easily biodegradable. Thus, PHAs are a promising biomaterial that can substitute the conventional plastics used widely nowadays. PHAs are accumulated by bacteria to serve as a reserve of energy, which they can access when they are under nutrient starvation. This phenomena allows the bacteria to survive adverse conditions which can occur in the gastrointestinal tract and thus, gain an advantage over other microorganisms. Knowledge about the PHAs accumulating bacteria and the functions they perform in the gastrointestinal microbiome can help the host stay healthy. Adding PHAs-accumulating bacteria at varying concentrations to fish food may influence positively on the fish growth. Moreover, PHAs-accumulating bacteria exhibit similar activity to probiotics. Therefore, PHAs-accumulating bacteria can be used as an alternative to traditional therapeutics like antibiotics.

The study will be performed using Next Generation Sequencing (NGS), the technique based on the nucleotide structure DNA analysis. To characterize the gut microbiomes of the fish, the fragments of *16S rRNA* gene belonging to bacteria DNA will be analyzed.

The main objectives of the proposal are:

- to determine the basic knowledge about the structure of the microbiome in the gastrointestinal tract of tench;
- to compare the microbiotas of wild and farmed fish;
- to detect PHAs-accumulating bacteria in the microbiome of tench;
- to determine whether the presence of PHAs-accumulating bacteria affect the overall structure of the microbiome.

This study will not only provide the fundamental knowledge about the composition of the microbiome in the gut of tench but will also create opportunity to use this knowledge in practice, such as biomanipulation of the microbiome to increase the efficiency of food utilization and to reduce the negative effects of the diseases in fish.