

Bioinformatic modelling of the impact of probiotic supplementation on microbiomes of breeding ponds and of digestive tract of the Common carp (*Cyprinus carpio*)

In recent years, there is great interest in the use of effective microorganisms as probiotic supplementation in aquaculture in order to improve water quality, inhibit pathogens and promote growth of farmed fish. The use of probiotics, which control pathogens through a variety of mechanisms is viewed as an alternative to antibiotics and has become a major field in the development of aquaculture. Considering the potential benefits of adding probiotics, many farmers have recently been using commercially available products in their fish farms. The concept of effective microorganisms was primarily developed in Japan by Dr. Teruo Higa, who proposed a consortium of beneficial and naturally occurring lactic acid bacteria, phototrophic bacteria, actinomycetes, yeasts and fermenting fungi, composed of over 80 microorganism species, as a solution to the restoration of a healthy ecosystem in soil and water. The two potential major benefits of probiotic supplementation in aquaculture are the improvement of feed efficiency achieved by providing additional digestive enzymes and increased disease resistance by competitive exclusion or growth inhibition of pathogenic species

However, there are very few studies related to the administration of probiotics in the Common carp, especially when probiotics are implemented as a mixture of effective microorganism communities into breeding ponds and not as a particular bacteria species in experimental tanks. Therefore, the goal of our project is to analyse the impact of probiotic supplementation of pond water fish and feed on the microbiome of fish digestive tract. During the first year of the project we conduct an aquaculture experiment using five constellations of experimental conditions: (1) no probiotic supplementation, (2) probiotic supplementation of water with supplement A, (3) probiotic supplementation of water with supplement B, (4) probiotic supplementation of water with supplement A and probiotic supplementation of feed, (5) probiotic supplementation of water with supplement B and probiotic supplementation of feed. Then, during the next three years we will apply bioinformatic methods to model: (1) changes in water microbiome over time, (2) changes in the microbiome of pond sediment over time and (3) the correlations between these two microbial communities, (4) differences in water microbiomes between experimental conditions, (5) differences in pond sediment microbiomes between experimental conditions, (6) differences in fish intestinum microbiomes between experimental conditions, (7) differences in water microbiome products (expressed by microbiotic genes expression) between experimental conditions.

The expected outcome of our project is the better understanding of changes in microbiome diversity expressed as the number of bacteria and their abundance. We will consider changes of diversity in time (three time-points of water and sediment sample collection during the production year) and due to different probiotic supplementation schemes (five experimental conditions). This will be analysed on the environmental level - by considering microbiomes of pond water and sediment and on the host level - by considering how/if fish intestinal microbiome is dependent on environment. Another, aspect which will emerge from the analyses is the knowledge to which extend water microbiome biological diversity expressed by bacterial DNA reflects functional diversity expressed by microbial gene expression based on the RNA analysis.