It is clearly understood that cyanophages plays an important role in chemical elements circulation in the nature. Cyanobacteria are organisms absorbing carbon from the atmosphere. Cyanobacterial cells killed by cyanophages release organic compounds into the water environment which can be utilized by phytoplankton or moved into the benthal sediment through the biological pump. The release of dissolved organic matter after viral-induced cell lysis modulates global biogeochemical cycles and influences actively on the microbial composition dynamic. In addition, viruses can also change the productivity and diversity of ecosystems through the horizontal gene transfer or/and the expression of viral-encoded auxiliary metabolic genes (AMGs). Through the modification of host's metabolism, cyanophages can modulate rates of synthesis and consumption of selected metabolites which has an impact on higher trophic levels. Despite constituting an important trophic link, cyanophages are relatively poorly understood.

Many marine cyanophages carry AMGs, which are highly expressed during the infection and ensure the production of ATP and reducing equivalents as well as supply of nucleotide precursors required for genome replication and phage protein synthesis.

Unlike marine cyanophages, freshwater cyanophages (with some rare exceptions) possess far fewer AMGs, too few to modify actively the host's metabolism on the genetic level. Despite the lack of AMGs, freshwater cyanophages can significantly alter the metabolic pathways affecting concentrations and cycling of the intracellular compounds. This suggests a tighter correlation between freshwater cyanophage replication and the host transcription machinery in comparison to marine cyanophage and cyanobacterial systems. However, these conclusions are based mainly on genome analysis and some transcriptomic research thus should be verified experimentally. The model of changes in metabolism caused by viral infection in freshwater cyanobacteria is still unknown. Therefore, there is a need for more studies simultaneously examining both the extent to which cyanophages affect host gene expression, protein synthesis and degradation, and the production of specific metabolites.

The project combines a set of laboratory-based experiments using modern methods. Proteom is a set of proteins present in cells. Differences in the composition of these proteins will be determined by two-dimensional difference gel electrophoresis (2D DIGE), and the identification of proteins will be performed using liquid chromatography coupled with tandem mass spectrometry (LC-MS/MS). RNA sequencing will provide a profile of changes in the transciptome, in the expression level of all genes in the cell. Proteomic and transcriptomic profiles will allow identification of metabolic processes that have been altered as a result of viral infection. The obtained results will be confirmed using LC-MS/MS by quantifying selected metabolites that are intermediates or end products of the pathways of interest. These studies will be complemented by physiological analyzes covering chlorophyll fluorescence, gas exchange, and other basic physiological parameters. By bringing together data from all parts of the project, the study will provide insights into how freshwater cyanophages manage the host metabolism.

The successful implementation of the work plan and achievement of the project goals will provide the first-ever comprehensive analysis of the cyanobacterial infection process. By filling the gaps in this field which constitutes a great scientific challenge, the improvement of ecological models will be possible. Furthermore, it will provide the benefits and obstacles associated with the development of more efficient strategies to reduce the occurrence of toxic cyanobacterial blooms. In the longer term, a thorough understanding of the mechanism of cyanophage infection could help develop a cyanobacterial transduction method that will improve the genetic engineering of these organisms. The results of our research have a chance to become a milestone in the study of cyanobacteria.