Cyanophages (viruses infecting cyanobacteria) are considered to be key players in structuring microbial communities due to their host-specificity, ability to suppress host metabolism and growth, and subsequent lysis of host cells after completion of their viral replication. Yet we know practically nothing about how cyanophage-cyanobacterium interactions influence interspecies relationships (e.g., competition between two cyanobacterial species) and their dynamics within the community. Using bloom-forming freshwater cyanobacteria as a model system we propose to study the interactions between ecologically important species and the cyanophages that infect them to gain an understanding of the mechanisms through which viruses influences cyanobacterial bloom dynamics. We aim to assess how and to what extent cyanophage infection and lysis contributes to i) the carbon and energy flow in the infected/resistant cyanobacterial strains; ii) the shift in species composition and dominant taxa resulting in the modification of cyanobacterial blooms composition and dynamic. The project will combine a set of laboratory-based co-cultivation experiments and field sampling campaigns supplemented by sophisticated bioinformatics and statistical methods. The study will provide insights into how cyaophage-cyanobacteria interactions influence cyanobacteria community diversity and succession. This is important for both, the fundamental understanding of the functioning of the lower part (microbial) food web and for the practical applications of risk assessment and management of harmful freshwater cyanobacterial blooms. Furthermore, this study has a potential for uncovering previously unrecognised mechanisms of virus-host-competitor relationships, which will improve our fundamental knowledge about the functioning of the aquatic microbial food webs.