

The goal of this project is to define how the specific environment of mammalian gastrointestinal tract may have shaped the evolution of the protein composition of T4 phage head.

Bacteriophages are naturally present in human and animal organisms and they constitute an important, yet still underappreciated, part of our microbiome. They may regulate our bacterial microflora and possibly even modulate our immune responses. Bacteriophages are particularly abundant in human gastrointestinal tract. Therefore, it appears reasonable to suspect that the specific characteristics of human gastrointestinal tract – such as extremely acidic or alkaline pH and exposure to bile and digestive enzymes – may have played a major role in phage evolution. Bacteriophage T4 is one of model phages and it has been thoroughly characterized when it comes to its structure, genetics and interactions with its bacterial host. However, the data regarding its evolution in the context of evolutionary response to selection pressure of its natural environment are scarce.

In this project, we aim to generate a complete panel of T4 phage mutants with altered head composition and subsequently conduct a comparative analysis of those mutants regarding (I) their survival in mammalian gastrointestinal tract, and (II) their susceptibility to highly acidic or alkaline pH, bile salts and activity of proteolytic digestive enzymes. Results of the project will allow us to identify a link between certain head proteins and phage survival in the segments of gastrointestinal tract and, as an effect, to gain better understanding of the evolution of phages as a part of our microbiome.