

# Bacteriophage biodiversity

CJS INRA ELIGIBLE\*

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Laboratory

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Subjects / Tools-Methodologies

- 1 : distant homologs of phage proteins/informatics
- 2 : estimation of diversity rates and rules/informatics, phylogeny
- 3 : in vivo analysis of new phage functions/virology, molecular biology

\* CJS INRA eligible : available funding

This project may be selected to be founded by a 5-year grant from INRA (Early stage scientist contract)

Summary of lab's interests

The Thesis will be developed in the frame of a collaboration between two teams "Dynamics of bacteriophage genomes" (Micalis, INRA, France), and "Genomes bioinformatics laboratory" (ULB, Belgium). The french team is a team of biologists essentially, interested in understanding the molecular basis of the high flexibility of temperate phage genomes, and in studying the impact of this remarkable evolvability of phages on bacterial populations in complex ecosystems, such as the gut microbiote. The belgian team is a team of computer scientists, specialised in the study and classification of mobile genetic elements. It has recently proposed a network classification of phages, and has developed a platform for the analysis of such mobile elements, named ACLAME.

Summary of project

Phage genomes are full of genes of unknown functions, which makes research on these objects difficult. This poverty could be due either to the fact that phage genes rarely have common ancestry, or that they have common ancestry but recombination and mutagenesis rates are so high that they blurr the signal. We challenged the second hypothesis, by fine-tuning the presently available sophisticated programs for distant homology searches, and found evidence, for at least a first family of phage proteins, that ancestry is indeed present (Lopes et al., NAR 2010). This study paves the way for a systematic approach allowing detection of new families of distant homologs among phage proteins. This will be the starting point of the thesis project, which is aimed at leading to i) the uncovering of rules governing phage protein evolution, and ii) the uncovering of interesting new functions, and their experimental validation at the bench. The phage genomes are a good field for such an analysis, because many complete genomes are available (550 at present, plus 1200 prophages), and each genome contains a limited amount of genes