Choreography of phages PAK-P3 and PhiKZ genomes during Pseudomonas aeruginosa infection.

Amaury Bignaud*[1], Quentin Lamy-Besnier[2,3], Romain Koszul , Laurent Debarbieux , and Martial Marbouty

[1]Regulation Spatiale des Genomes – Institut Pasteur de Paris – France
[2]Bacteriophage, Bacterium, Host Laboratory, Department of Microbiology, Institut Pasteur, Paris – Institut Pasteur de Paris – France
[3]Université de Paris, Paris, France – Université de Paris – France

Résumé

If bacteria appears to be the most diverse cellular domain of life on earth, they are outnumbered by the viruses that can infect them. With an estimation of 10^31 particles, bacteriophages (phages) are the most abundant genomic entities across all habitats and a major reservoir of genetic diversity. Up to date, the vast majority of sequenced phage genomes are dsDNA and smaller than 100kb. In recent years, several publications have expanded our understanding of phages biodiversity and demonstrate the existence of phages with large genomes, rising numerous questions concerning how these genomes folds within their capsid but also during their infection cycle. Recently, a study proves the existence of a compartment that separated viral DNA from the cytoplasm in *Pseudomonas chlororaphis* phage 201phi2 and demonstrates that large phages have developed innovative mechanisms to succeed in their infection cycle. Large phages typically contain more genes implicated in genome replication, nucleotide metabolism or coding for DNA binding proteins and could, therefore, have developed new strategies concerning their 3D genome organization and the hijacking their host. To tackle this question, we have used chromosome conformation capture (HiC) to characterize the phage-host genomes interactions during the infection of *Pseudomonas aeruginosa* by two different phages, PAK-P3 and phiKZ (PAK-P3 is a 88kb virulent phage, and phiKZ is a 280kb giant bacteriophage). We performed a kinetic of both infection cycles and followed, concomitantly, the variation of genomes architecture through time. Our data show a correlation between variations in phages genomes folding and its transcriptional program. In parallel, we observed a global disorganization in the host genome, with a decreasing of the signal of the observed borders in the genome. Our results demonstrate that phages are highly dynamics genomic entities when they are active and pave the way to in-depth analysis of their infection cycle.

Mots-Clés: HiC, nucleus, like, jumbo phage, bacterial infection

*Intervenant