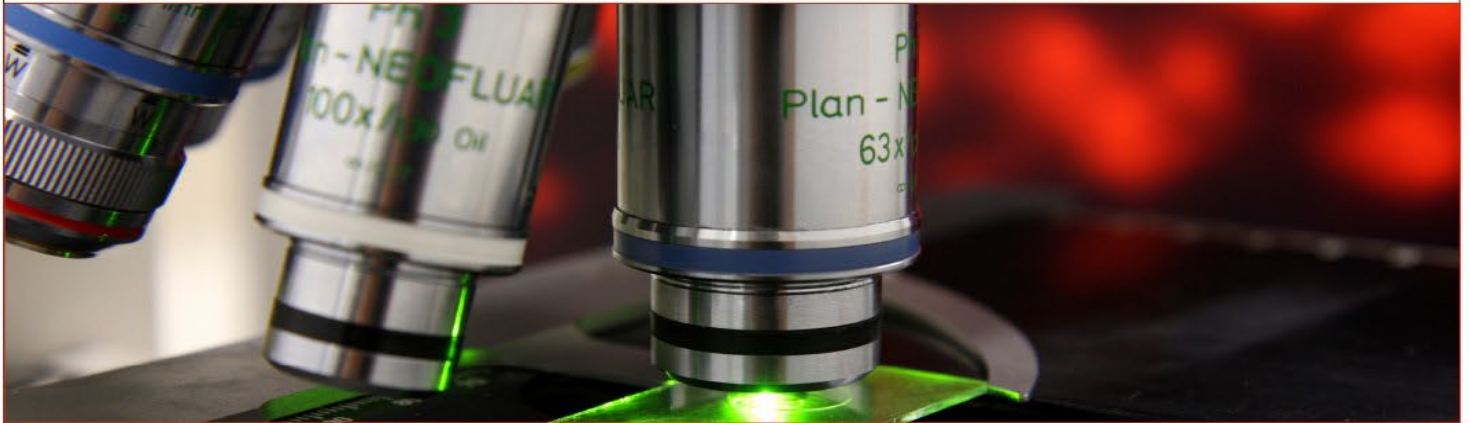


SÉMINAIRES ET CONFÉRENCES



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“Microscopic Battle: Discovering Phages and Bacteria in Their Natural Habita”

Facing the therapeutic impasse of antibiotics, farming systems, including aquaculture, should consider the extraordinary resource of phages, natural bacterial predators, for environmentally friendly practices. Sustainable and safe use of phages requires an understanding of their specificity and evolution. However, our knowledge of phage infection mechanisms is mainly based on model systems in laboratory conditions, which do not reflect the enormous diversity that exists in nature.

Using natural populations of marine bacteria (vibrios) infecting oysters, we have shown that most phages have a narrow host range. Their specificity depends first on their ability to bind to the host surface and second on their capacity to resist intracellular defense mechanisms. In the case of the oyster pathogen *Vibrio crassostreae*, we can track coevolutionary lineages in the marine environment. These are phage species capable of adsorbing specifically to clades nested within *V. crassostreae*. I will present preliminary results from a follow-up of these lineages in a new time-series sampling and genomic analyses that allow us to propose evolutionary scenarios.

Emerging resistance to phages in nature primarily results from horizontal gene transfer. We have discovered a family of phage satellites, named Phage-Inducible Chromosomal Minimalist Islands (PICMIs), which are widely distributed in the Vibrionaceae family. PICMIs are characterized by their reduced gene content, lack of genes for capsid remodeling, and the packaging of their DNA as a concatemer. These islands integrate into the bacterial host genome adjacent to the *fis* regulator and encode three core proteins essential for excision and replication. PICMIs rely on virulent phage particles to spread to other bacteria and protect their hosts from competitive phages without interfering with their helper phage. The discovery of PICMIs highlights the necessity of fully characterizing virulent phages and their host producers to prevent the spread of satellite-mediated resistance in phage therapy.

In conclusion, exploring natural populations of phages and bacteria is essential for developing fundamental knowledge, providing a solid basis for informed consideration of new therapeutic avenues in the fight against pathogens, while preserving the delicate balance of the microbial ecosystem.



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