Coevolution and competition drive the diversification of CRISPR immunity

Martin Guillemet, Hélène Chabas, Antoine Nicot, François Gatchich, Enrique Ortega-Abboud, Cornelia Buus, Lotte Hindhede, Geneviève Rousseau, Thomas Bataillon, Sylvain Moineau, Sylvain Gandon

CEFE UMR 5175, CNRS - Université de Montpellier

Host resistance diversity reduces the emergence and the evolution of pathogens. But it is unclear what drives the dynamics of this diversity. Here we study a coevolving phage population on the diversification of bacterial/host CRISPR immunity across space and time. We find that the negative-frequency-dependent selection generated by coevolution is a powerful force that maintains host resistance diversity and selects for new resistance mutations. But we also find that host evolution is driven by asymmetries in competitive abilities among different host genotypes. The fittest host genotypes are targeted by the evolving phage but they are also the ones that acquire faster new CRISPR resistances. Our study reveals the interplay between intraspecific and interspecific interactions on the evolutionary dynamics of host resistance diversity. The recognition of the joint impact of competition and coevolution on host resistance diversification challenges coevolutionary theory and has long-term implications on the evolution of interacting species.

1. What is your pathogen? Multiple options possible (e.g. if working on coinfections)

**Other viruses**: Bacteriophage 2972

**Bacteria**: Streptococcus thermophilus

2. On a scale of 1-5 is your work mostly eco/epidemiological or evolutionary? 3

3. On a scale of 1-5 is your work mostly theoretical or experimental/empirical?
   5 (100% empirical)