
Modelling eco-evolutionary interactions between bacteria and bacteriophages

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Résumé

Bacteriophages are one of the most ubiquitous entities in nature and play a crucial role in the dynamics of microbial communities. They can act both as bacterial predators, directly shaping which bacterial species are present in the environment, and also as drivers of horizontal gene transfer, promoting the dissemination of adaptive traits through transduction. An extensive amount of work has been done, both experimentally and theoretically, to understand the conditions in which certain bacterial species are favoured or disfavoured by the presence of bacteriophages. Nevertheless, it is difficult to study the role of the different mechanisms involved in the interactions between bacteria and bacteriophages, particularly in ecologically complex scenarios, where spatial structure can greatly influence the dynamics of the communities.

We developed an ecological and evolutionary individual-based model to better understand the impact of bacteriophages in microbial communities. Each bacteria and bacteriophage are explicitly modelled, and we are able to track the fate and individual behaviours of each cell, their adaptation at the genomic and phenotypic level and the stochasticity inherent to the genetic mechanisms underlying their interactions. Our model recovers the typical observed dynamics of bacteria-bacteriophage interactions, whilst simultaneously predicting the outcome of more ecologically complex scenarios of adaptation. In particular, we simulate the dynamics of phage predation in spatially distributed communities, the different roles of lysogeny in these communities, and the effect of transduction in bacterial adaptation.

The mechanistic-based theoretical approach we propose here can be inspired by results from experimental approaches and comparative genomics, but it can also guide further research. It is an important step to integrate the different scales involved in the study of bacteria-phage interactions, from the individual molecular processes to the collective, community level dynamics. Such integrative approaches will be fundamental to disentangle these interactions and their consequences for microbial communities and public health.

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